

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 00:14:24 ; Search time 52.75 Seconds
(without alignments)
514.873 Million cell updates/sec

Title: US-09-670-568B-1

Perfect score: 2383
Sequence: 1 MSQSTQTEFLSPSEVFQHIW.....PKSDVFRHSPKPRRSYYP 448

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A.Geneseq_0601.*
1: /cgnl_9/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /cgnl_9/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /cgnl_9/gcgdata/geneseq/geneseq/AA1982.DAT.*
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6: /cgnl_9/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /cgnl_9/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /cgnl_9/gcgdata/geneseq/geneseq/AA1987.DAT.*
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11: /cgnl_9/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /cgnl_9/gcgdata/geneseq/geneseq/AA1991.DAT.*
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14: /cgnl_9/gcgdata/geneseq/geneseq/AA1993.DAT.*
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19: /cgnl_9/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /cgnl_9/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /cgnl_9/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /cgnl_9/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2383	100.0	448	20	AAV45246
2	2383	100.0	448	20	AAV05958
3	2383	100.0	448	21	AAAB11359
4	2296	96.3	483	20	AAV05961
5	2185	91.7	516	20	AAV05954
6	2185	91.7	516	21	AAAB11363
7	2185	91.7	641	20	AAV45247
8	2185	91.7	641	20	AAV05953
9	2185	91.7	641	21	AAAB11358
10	2185	91.7	680	21	AAAB11361
11	2185	91.7	680	21	AAV50997

12	2169	91.0	680	20	AAV05958	Human cell regulat
13	2169	91.0	680	21	AAV50998	Rat KET protein.
14	2011	84.4	393	20	AAV05957	Human cell regulat
15	1938	81.3	389	20	AAV05964	Mouse cell regulat
16	1813	76.1	461	21	AAAB11362	Human p53 regulat
17	1813	76.1	586	20	AAV05956	Human cell regulat
18	1811	76.0	461	20	AAV05963	Mouse cell regulat
19	1811	76.0	586	20	AAV05962	Mouse cell regulat
20	1796	75.4	356	20	AAV43135	Human p40 protein
21	1796	75.4	356	21	AAAB11360	Human p63 protein
22	1796	75.4	586	21	AAAB11357	Human p63 protein
23	1789	75.1	586	20	AAV41032	Human lung tumor a
24	1789	75.1	586	21	AAAB11317	Human lung cancer-
25	1297.5	54.4	499	21	AAV44635	Human p53 tumor s
26	1297.5	54.4	499	21	AAV44635	Human p53 beta sp
27	1287.5	54.4	635	20	AAV30661	Human NBS-1 alpha
28	1287.5	54.4	636	18	AAV36184	Human p53 tumor s
29	1297.5	54.4	636	21	AAV44634	Human p73 alpha sp
30	1296.5	54.4	499	18	AAV36183	Monkey p53 tumor
31	1296.5	54.4	636	21	AAV50999	Monkey p53 protein.
32	1296.5	54.4	637	18	AAV36182	Monkey p53 tumor
33	1279.5	53.7	589	18	AAV36185	Mouse p53 tumor s
34	1251	52.5	506	18	AAV36188	Human p53 tumor s
35	1248.5	52.4	587	18	AAV36187	Human p53 tumor s
36	1248.5	52.4	588	18	AAV36189	Human p53 tumor s
37	722.5	30.3	393	20	AAV57244	Human p53 protein.
38	722.5	30.3	393	19	AAV84270	Human p53 protein.
39	717.5	30.1	355	18	AAV13950	De1356-393 modifie
40	717.5	30.1	363	18	AAV13954	Modified p53 varia
41	717.5	30.1	393	13	AAV22238	Sequence of 53 kd
42	717.5	30.1	393	13	AAV22238	p53. Synthetic.
43	717.5	30.1	393	16	AAV46223	p53 protein. Homo
44	717.5	30.1	393	16	AAV79658	Human p53 protein.
45	717.5	30.1	393	19	AAV48658	Amino acid sequenc

ALIGNMENTS

RESULT 1	
AAV45246	AAV45246 standard; Protein: 448 AA.
ID	AAV45246
XX	AAV45246;
AC	07-JAN-2000 (first entry)
XX	
DE	Human p51 protein A.
XX	
KW	Human: p51; p53 related gene; cell proliferation; regulation; cancer;
KW	tumor suppression; diagnosis.
XX	
OS	Homo sapiens.
XX	
FT	Key
FT	Domain
FT	Domain
FT	Domain
FT	Domain
FT	Domain
XX	
XX	W09950412-A1.
XX	
XX	07-OCT-1999.
PD	
XX	
XX	24-MAR-1999;
XX	99MO-JP01512.
XX	
PR	27-MAR-1998;
XX	98JP-0100467.
XX	
PA	(SAKA) OTSUKA PHARM CO LTD.
PA	(IKAWA/) IKAWA Y.
XX	

PI	Ikawa Y, Ikawa S, Oblinata M;
XX	
DR	WPI: 1999-591318/50.
DR	N-PISDB: AA625770.
XX	
PT	New p53 related human gene p51, useful for diagnosis, investigation and
PT	treatment of cancers and screening for potential cell proliferation
PT	agents -
XX	
PS	Claim 1: page 147-148; 163pp; Japanese.
XX	
CC	The present sequence represents a human p51 protein, which is related to
CC	p53 and has cell proliferation regulation and tumour suppression
CC	activity. The p51 gene can be used in the investigation, diagnosis and
CC	treatment of diseases such as cancer, with which the p53 family cell
CC	proliferation regulation is associated. The p51 protein may be used for
CC	screening potential agonists and antagonists of its regulatory function,
XX	for use as drugs,
XX	
SO	Sequence 448 AA;

Query Match	100.0%	Score 2383	DB 20	Length 448
Best Local Similarity	100.0%	Preg. NO. 2	1e 207	
Matches 448; Conservative	0	Mismatches	0	Gaps 0

QY	1	MSOSOTNEFISPEYFOHIMFOLEBPICISVOPIDLNFDSESDGATKIEISMDCI	60
Db	1	msqsqctneiflisspevfqhlwtdllegpilsctvsygidlnfvdepesdgatunkieismdc	60
QY	61	DSDSLDPMMQYOTNLGLNSMDQOIONCSSSPNTHAONSNWATAPVAQPSSTDAL	120
Db	61	dsdlsdpmwpytngllnsmndqqlngssstspncthaqnsvrlapsyqpsstdal	120
QY	121	SPSPAISENTDPCGHSHSDVSFOOSSTAKSATMTYSTELKILYQIAKTCPIQIKVMT	180
Db	121	spspsaisntdypghsfdsvfqgstaksatwystelkilyqiaktcpiqikvmt	180
QY	181	POGAVIRAMPYKKAHEHTEVYKACPNHELSRENEGOIAPSHLIRVEGNSHAQYEDP	240
Db	181	pgavirampykaaehvtevykacpnhelestneogiapshlirvegnsahqyedp	240
QY	241	ITGRQSVLVPEYEPPOVGTETFTVLNFMCSNCCVCGNMRRPILITVLETRDGOVLE	300
Db	241	itgrqsvlvpeypvgvgtftvlynfmcsncvgnmrrpilitvletrdgvlgtrc	300
QY	301	FEARICACPGDRADBDSDIRKQOVSSTKNGDSTKRRPFONTHGIDWTSIKRRSPDDE	360
Db	301	featiccpgardraddesdtrkqvsdstkngdtklrrpfqntbqilqmtsikkrrspdde	360
QY	361	LILYVPRGRETTEMLIKESLELMQULPOHTIETERYQOQOQOQHONHLOKHLISACFR	420
Db	361	lilyvprgrettelmlikeslelmqulpohtieteryqoqoqoqhonhlokhlisacfr	420
QY	421	LVEPRRETPKOSDOEFPHSKPMPNRSYVP	448
Db	421	lvpeprretpkosdovfphskpmpnrsvyp	448

RESULT	2
AAV05955	
ID	AAV05955
xy	standard; Protein; 448 AA.

DT 16-AUG-1999 (first entry)
YY

XX		Cell regulatory protein; p63; huTap63 gamma; Tap63 gamma; human
XK		cancer; tumour suppressor; cell cycle control; apoptosis;
KM		cell proliferation; cell differentiation; therapy.
KW		
de	human cell regulatory protein p63, isoform huTap63 gamma.	

OS	Homo sapiens.	
XX		
PN	MO9919357-A2.	
XX		
PD	22-ADR-1999.	
XX		
PF	02-OCT-1998;	98MO-US21992.
XX		
PF	29 MAY 1998.	98US-0082716.
PR	15-OCT-1997;	97US-0062076.

PT New isolated p63 cell regulatory protein for, e.g. treatment of tumours

XX

PS

XX Claim 23; Fig 11; 16pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes. It was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta1 and gamma forms, where the delta1 form lacks the transactivation domain. The present sequence represents human p63 isoform TP63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta1 isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AA05953-66), polynucleotides (see AA05872-83) and anti-p63 antibodies (see AA05953-66) can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Query Match	100.0%;	Score 2383;	DB 20;	Length 448;
Best Local Similarity	100.0%;	Pred. No. 2.1e-207;		
Matches 448;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MSQSTQTNFELSPEVFOHIMDFLEKOPICISVOPJDLNPNVDEPSDQATKITEISMDCI	RMQ	60
Db	1	msqstqtnfelspevfqhlmflefleqpcrcsqvldlnpnvdepsdqatktelsmdcirmq		60
QY	61	DSLISPMPMQPTNLGLNSKSDQOIQNGSSSTSPYMTDAQNSVTAPSPYAQSPSTEDAL		120
Db	61	dslislpmpmqptnlglnsmndqdlqngssstspyltdhaqnsvtapsypaqspstfdal		120
QY	121	SPSPAIPSNTDYPGHSFEDVSFOQSSPAKATWTYSTELKRYCOIATCTPQIKWMTTP		180
Db	121	spspaipnsntdypghsfedvsfqsstakawtystelkrycoiatctpqiakwmtpp		180
QY	181	PGAVIIRAMPYRKKAEHYTEVVKRCRNHELSPFNCGQIAPPSHLIRVGNASHQAYEDP		240
Db	181	pgavirampyrkkaehytevvrkrcrnhelspfnecqiappshlirvgnashqayedp		240

Db 181 pggavirampyxxkaehlevvkrcpnhejsrefneqgiappshllirvegnshaqyvedp 240
 QY 241 ITGKQSVLVPEPPQVGTFTTLYLNFMCNNSCVGGMNRRPILITVLETDGVLGRRC 300
 Db 241 itgqsvlvpeppqvgtfttlylnfmcnscvvgmmrrpiliivltetdgvlgrrc 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRRONTGHIOWTSIKRRSPDE 360
 Db 301 fearicacpgdrkadedsirkqovsdstknkgdtkrpfrrnhtgihqmtsikkrrspde 360
 QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPHQHTIFTYRQOQOQOHLQKHLISACFRNE 420
 Db 361 llylpvgrgretylemllkikeslelmqylpqhtletyrgqgqghhllqkhlisacfrne 420
 QY 421 LVEPRRETPKQSDVFFRRSKPPNRSVYP 448
 Db 421 lveprretpkgsdvffrrskppnrsvyp 448

RESULT 3

AAB1359

ID AAB1359 standard; Protein; 448 AA.

AC AAB1359;

DT 21-FEB-2001 (first entry)

DE Human p63 protein isoform #3.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KM vaccine; detection.

OS Homo sapiens.

PN W0200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000MO-US089896.

PR 02-APR-1999; 9905-0285479.

PR 17-DEC-1999; 9905-0466396.

PR 30-DEC-1999; 9905-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

XX WPI: 2000-628399/60.

DR N-PSDB; AAC66029.

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XX

Query Match 100.0%; Score 2383; DB 21; Length 448;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-207;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSQSTQINELISPEVFOHIMWLEDPICSVOPIDLNVEPSEDEGATNKIEISMDCTRMQ 60
 Db 1 msqstqinelispevfqhlmwleqpicsvopidlnfvepsedegatkiesmdctirmq 60
 QY 61 DSDLSDPMMQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPVAPQSPSTDAL 120
 Db 61 dsdlsdpmmqytnlglnsmdqoinqssstspynthaqnsvtlapsvqpsstidal 120
 QY 121 SPSPAIPESENTDYPGPHSPDYVFOOSSTFAKSATWYSTELKLYCOIAKTCPIQIKVMTTP 180
 Db 121 spspaipeentdypphspdyvfoosstfaksatwystelklycoiaktcpiqikvmttp 180
 QY 181 PGAVIRAMPYXXKAHEHTEVVKRCPNHELSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 Db 181 pggavirampyxxkaehlevvkrcpnhejsrefneqgiappshllirvegnshaqyvedp 240
 QY 241 ITGKQSVLVPEPPQVGTFTTLYLNFMCNNSCVGGMNRRPILITVLETDGVLGRRC 300
 Db 241 itgqsvlvpeppqvgtfttlylnfmcnscvvgmmrrpiliivltetdgvlgrrc 300
 QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDGTKRPFRRONTGHIOWTSIKRRSPDE 360
 Db 301 fearicacpgdrkadedsirkqovsdstknkgdtkrpfrrnhtgihqmtsikkrrspde 360
 QY 361 LLYLPVGRGRTYEMLLKIKESLELMQYLPHQHTIFTYRQOQOQOHLQKHLISACFRNE 420
 Db 361 llylpvgrgretylemllkikeslelmqylpqhtletyrgqgqghhllqkhlisacfrne 420
 QY 421 LVEPRRETPKQSDVFFRRSKPPNRSVYP 448
 Db 421 lveprretpkgsdvffrrskppnrsvyp 448

RESULT 4

AAV05961

ID AAV05961 standard; Protein; 483 AA.

AC AAV05961;

DT 16-AUG-1999 (first entry)

DE Mouse cell regulatory protein p63, isoform mutAp63 gamma.

KW Cell regulatory protein; p63; mutAp63 gamma; TAp63 gamma; mouse;
 KM cancer; tumour suppressor; cell cycle control; apoptosis;
 XX cell proliferation; cell differentiation; therapy.

OS Mus sp.

PN W09919357-A2.

PD 22-APR-1999.

PF 02-OCT-1998; 98WO-US21992.

PR 29-MAY-1998; 98US-0087216.

PR 15-OCT-1997; 97US-0062076.

PA (HARD) HARVARD COLLEGE.

PI McKeon F, Yang A;

XX WPI: 1999-277595/23.

DR N-PSDB; AAX58580.

XX

XX

XX

XX

New isolated p63 cell regulatory protein for, e.g. treatment of
 tumours

PS Claim 23; Fig 17; 161pp; English.

XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
CC RACE. Sequencing of the amplification product indicated that the
CC amplified cDNA possessed a truncated N-terminus, i.e. the
CC transactivation domain was absent. Additional splice variants were
CC identified by screening a cDNA library with a probe corresponding
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
CC variants differing at the C-terminus are designated as alpha, beta
CC and gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents murine
CC p53 isotype mutap63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

XX Sequence 483 AA;

XX Query Match 96.3%; Score 2296; DB 20; Length 483;

XX Best Local Similarity 96.9%; Pred. No. 1.8e-199;

XX Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLNFVDEPSEDGATNKIETISMDCIIMQ 60
DB 40 msqstqetseflspvfgqhlwdfleqpsvqplnfdfvdepgatnkietismdcimq 99
QY 61 DSDLSDPKMPQYTNIGLNSMDQIQNGSSSTSPYNTHAQNSVATAPRYAQPSTFIAL 120
DB 100 dsdlsdpmqpytniglnsmdqiqngssstspynthaqnsvatapyqpsstfial 159
QY 121 SSPAPSPNTDVPGRHSDVSPQOSTAKSATWTSTELKRLKYCOIATKCPRIQIKVTMP 180
DB 160 spsapspntdvpgrhsvdvsfqsqstakstwtstelkrlkycoiatkcpriqikvmtpp 219
QY 181 PGQAVIRAMPYKKAHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
DB 220 pgqavirampyvkkaehylevkrpcpnhelsefnegoiappshlirvegnsahayvedp 279
QY 241 ITGROSVLVPRPPOVGFETVLTNPMCNSSCVGMNRPLITVLTETPRGVLGRRC 300
DB 280 itgrsvlvprppovgfeftvltynpmcnsscvgmnrplltvltetrgvlgrrc 339
QY 301 FEARICACGPRKADKDESIKQOVSSTKNGDGTKRPFQNTHGIGMTSIIKRRSPDE 360
DB 340 fearicacgprkadedsiirkqovsdstkngdgtkrpfqntthgigmtsiikrrspde 395
QY 361 LLYLPVGRGRTYEMILKTESLMOYLPORITETRYROOQOOHOLLOKHLISCFRNE 420
DB 396 llylpvgrgretymilktesiemoyporitetryrooqooohollokhlisacfne 455
QY 421 LVEPRREPQKSDVFFRHSKPPNRSVYP 448
DB 456 lveprrepqksdvffrhnppnhsyyp 483

RESULT 5
AAY05954
ID AAY05954 standard; Protein; 516 AA.

XX AC AAY05954;

XX DT 16-AUG-1999 (first entry)

XX DE Human cell regulatory protein p63, isoform huTAP63 beta.

XX KW Cell regulatory protein; p63; huTAP63 beta; TAP63 beta; human;

XX KW cancer; tumour suppressor; cell cycle control; apoptosis;

XX KW cell proliferation; cell differentiation; therapy.

XX OS Homo sapiens.

XX PN MO9919357-A2.

XX PD 22-APR-1999.

XX PF 02-OCT-1998; 98MO-US21992.

XX PR 29-MAY-1998; 98US-0087216.

XX PR 15-OCT-1997; 97US-0062076.

XX PA (HARD) HARVARD COLLEGE.

XX PI MCKEON F, Yang A;

XX DR WPI: 1999-277595/23.

XX DR N-PSDB; AAX58573.

XX PT New isolated p63 cell regulatory protein for, e.g. treatment of

XX PT tumours

XX PS Claim 23; Fig 10; 161pp; English.

CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents human
CC p63 isotype TAP63 beta. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

XX Sequence 516 AA;

XX Query Match 91.7%; Score 2185; DB 20; Length 516;

XX Best Local Similarity 94.1%; Pred. No. 2.2e-189;

XX Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSOSTOTNEFLSPEVFOHIMDFLEOPICSVOPIDLNFVDEPSEDGATNKIETISMDCIIMQ 60
DB 1 msqstqetseflspvfgqhlwdfleqpsvqplnfdfvdepgatnkietismdcimq 60

```

OY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 dsdlsdpmpqytnlglinsmdqiongssstspynldhagnsvtapsyaqpsstfdal 120
OY 121 SPSPALPSNTDYGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 spspalpsntdygphsfdvsfoqssstaksatwtystelklycoiaktcpdqikvmttpp 180
OY 181 PGCAVIRAMPYVYKKAHVTEVVKRCPNHLELSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 pgcavirampvykkaehvtevkrcpnhelelsrefneqiaappshllirvegnsahqyvedp 240
OY 241 ITGKQSVLYVEPPQVTEFTTVLYNFMCSNCCVGMNRRPILITVLERDGOVGLRRC 300
DB 241 itgqsvlyveppqvtefttvlynfmcnsscvgmmrrpiliivlelctrdgqvglrcc 300
OY 301 FEARICACPGDRKADDSIRKQOVSDSTKNGDGTAKRPFRONTHTGIOMTSIKRRSPDDE 360
DB 301 fearicacpgdrkadedsirkgvdsstkngdgtkrpfrqntngtqmtsikrrspdde 360
OY 361 LLYLPVGRRETYEMLKIKESLEIMQYLPQHTTETTYRQOQOQOQHLLQKHLSACFRNE 420
DB 361 llylpvgrretyemllkikeslelmqylpqhtletyrgqgqgqhllqk----- 410
OY 421 LVEPRRETPKOSDVFRRSKRP 442
DB 421 -----qtsiqspssygnssp 426

```

RESULT 6

AAB11363
ID AAB11363 standard; Protein; 516 AA.

AC AAB11363;

DT 21-FEB-2001 (first entry)

DE Human p53 protein isoform #7.

KW Lung cancer: therapy; treatment; human; tumor; immunogenic; cytostatic;

KM vaccine; detection.

OS Homo sapiens.

PN MO200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000MO-0508896.

PR 02-APR-1999; 99US-0285479.

PR 17-DEC-1999; 99US-0466396.

PR 30-DEC-1999; 99US-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

XX N-PSDB; AAC66033.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor

XX protein is used for detecting and monitoring progression of lung cancer

XX in a patient -

XX Disclosure; Page 255-256; 261pp; English.

XX This invention describes a novel isolated polypeptide (I) which

XX comprising an immunogenic portion of a lung tumor protein or variant (P2)

XX which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.

XX Sequence 516 AA:

Query Match 91.7%; Score 2185; DB 21; Length 516;
Best Local Similarity 94.1%; Pred. No. 2.2e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```

OY 1 MSQSTQTFNEFLSPEVFOHIDFLEOPICSVQPIDLNFVDEPSEDEGATNKIEISMDCIRMO 60
DB 1 msqstqtfneflspevfqhldflegpicsvqpidlnfvdesedgatnkiesmdcirmg 60
OY 61 DSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDAL 120
DB 61 dsdlsdpmpqytnlglinsmdqiongssstspynldhagnsvtapsyaqpsstfdal 120
OY 121 SPSPALPSNTDYGPHSFDVSFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
DB 121 spspalpsntdygphsfdvsfoqssstaksatwtystelklycoiaktcpdqikvmttpp 180
OY 181 PGCAVIRAMPYVYKKAHVTEVVKRCPNHLELSREFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
DB 181 pgcavirampvykkaehvtevkrcpnhelelsrefneqiaappshllirvegnsahqyvedp 240
OY 241 ITGKQSVLYVEPPQVTEFTTVLYNFMCSNCCVGMNRRPILITVLERDGOVGLRRC 300
DB 241 itgqsvlyveppqvtefttvlynfmcnsscvgmmrrpiliivlelctrdgqvglrcc 300
OY 301 FEARICACPGDRKADDSIRKQOVSDSTKNGDGTAKRPFRONTHTGIOMTSIKRRSPDDE 360
DB 301 fearicacpgdrkadedsirkgvdsstkngdgtkrpfrqntngtqmtsikrrspdde 360
OY 361 LLYLPVGRRETYEMLKIKESLEIMQYLPQHTTETTYRQOQOQOQHLLQKHLSACFRNE 420
DB 361 llylpvgrretyemllkikeslelmqylpqhtletyrgqgqgqhllqk----- 410
OY 421 LVEPRRETPKOSDVFRRSKRP 442
DB 421 -----qtsiqspssygnssp 426

```

RESULT 7

AAY45247
ID AAY45247 standard; Protein; 641 AA.

AC AAY45247;

DT 07-JAN-2000 (first entry)

DE Human p51 protein B.

KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;

KM tumour suppression; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

XX FT Domain 1..59 /label= transactivation_domain

XX FT Domain 142..321 /label= DNA_binding_domain

XX FT Domain 353..397 /label= oligomerisation_domain

XX PN MO950412-A1.

XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-JP01512.
XX
XX 27-MAR-1998; 98JP-0100467.
XX
XX (SAKA) OTSUKA PHARM CO LTD.
XX (IKAWA/) IKAWA Y.
XX
XX Ikawa Y, Ikawa S, Ohtnata M;
XX
XX WPI: 1999-591318/50.
XX N-PSDB; AAZ25771.
XX
XX New p53 related human gene p51, useful for diagnosis, investigation and
XX treatment of cancers and screening for potential cell proliferation
XX agents -
XX
XX Example 1; Page 152-154; 163pp; Japanese.
XX
XX The present sequence represents a human p51 protein, which is related to
XX p53 and has cell proliferation regulation and tumour suppression
XX activity. The p51 gene can be used in the investigation, diagnosis and
XX treatment of diseases such as cancer, with which the p53 family cell
XX proliferation regulation is associated. The p51 protein may be used for
XX screening potential agonists and antagonists of its regulatory function,
XX for use as drugs,
XX
XX Sequence 641 AA;
XX

Query Match 91.7%; Score 2185; DB 20; Length 641;
Best Local Similarity 94.1%; Pred. No. 3e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNFELSPVFOHIMDFLEOPICSVOPIDLNFDPESEDGATKIEISMCIRMQ 60
DB 1 msgstqtnfslspvfohlmfdeopicsvopidlnfdpegedatnkietismcirmq 60
QY 61 DSDLSPPMPQPTNGLNSMDQIQNGSSSTSPYNTDHAONSVPAPSPYAPQSSTFDAL 120
DB 61 ddsldspmpqptnnglnsmdqiqngssstspynthdhaonsvappspypqssftfal 120
QY 121 SPSPAIPTNTDVGPHSPFVSFOGSTAKSATWYSTELKILCOIATCTCIQIKWTP 180
DB 121 spspaiptntdvgphspfvsgostaksatwystelkiklcoiactctciqikwtp 180
QY 181 PGNAVIRAMPYKKAHTEVVKRCPNHLSREFNEGOIAPPSHLIRVGNSHAQYEDP 240
DB 181 pgnavirampykkahtevvkrcpnhlsrefnegoiappshlirvgnshaqyvedp 240
QY 241 ITGRQSVLVEPPPOVGEFTTVLYNFMCNSSCYGGMRRILITVLETRDGVLRRC 300
DB 241 itgrqsvlvepppovgefttvlynfmcnsscvggmrrililtvletrdgvlgrrc 300
QY 301 FEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPFRONTGCIQMTSIRKRSPDDE 360
DB 301 fearicacpgdrkadeedsirkqvdsdstkngdgtkrpfrontgciqmtsirkrspdde 360
QY 361 LLYLPVGRREYEMLIKESLELMQYLPOHTTETTRQOOOQOHLLORHLLSACFRNE 420
DB 361 llylpvgrreyemlikeslelmqylpohthtetttrqoooqohllorhllsacfrne 420
QY 421 LVEPRRETPKQSDVFFRHSKRP 442
DB 421 lveprretpkosdvffrhrskrp 442
QY 441 -----qtsiqspssygnsepp 426
DB 441 -----qtsiqspssygnsepp 426

RESULT 8
AAV05953
ID AAV05953 standard; Protein; 641 AA.
XX

AC AAV05953;
XX
XX 16-AUG-1999 (first entry)
XX
XX Human cell regulatory protein p63, isoform hUTAP63 alpha.
XX
XX Cell regulatory protein; p63; hUTAP63 alpha; TAP63 alpha; human;
XX cancer; tumour suppressor; cell cycle control; apoptosis;
XX cell proliferation; cell differentiation; therapy.
XX
XX Homo sapiens.
XX
XX W09919357-A2.
XX
XX 22-APR-1999.
XX
XX 02-OCT-1998; 98WO-US21992.
XX
XX 29-MAY-1998; 98US-0087216.
XX 15-OCT-1997; 97US-0062076.
XX
XX (HARD) HARVARD COLLEGE.
XX
XX McKeon F, Yang A;
XX
XX WPI: 1999-277595/23.
XX N-PSDB; AAX58572.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
XX tumours
XX
XX Claim 23; Fig 9; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
XX cell regulatory proteins (CRPs) termed the p63 family of proteins,
XX which demonstrate certain sequence identity to known tumour
XX suppressor proteins p53 and p73. It has been observed that the
XX known exon and intron sizes for these 2 genes, and from
XX identify new members of this gene family using a PCR-based strategy
XX of amplifying 2 exons in a conserved domain and their intervening
XX intron. The human p53 gene was localised to chromosomal position
XX 3q27-29. At least 6 different isoforms exist. Splice variants
XX differing at the C-terminus have been designated as alpha, beta and
XX gamma forms, while p63 members differing in the N-terminus are
XX designated as delta and tau forms, where the delta form lacks the
XX transactivation domain. The present sequence represents human
XX p63 isoform TAP63 alpha. p63 was detected in a variety of
XX human and mouse tissue. It demonstrates remarkably divergent
XX activities, such as the ability to transactivate p53 reporter genes
XX and induce apoptosis. Cessation or down-regulation of p63 expression
XX may play a critical role in the process of cervical squamous
XX differentiation, both benign and neoplastic. Delta isoforms of p63
XX act as dominant negatives towards transactivation by p53 and p63.
XX cachexia) and neuronal differentiation and related degenerative
XX disorders. p63 polypeptides (see AAV05953-64), polynucleotides (see
XX AAX58572-83) and anti-p63 antibodies of the invention can be used to
XX identify compounds useful for treating disorders involving such
XX processes, in detection and diagnosis, and in the production of
XX transgenic animals.
XX
XX Sequence 641 AA;
XX

Query Match 91.7%; Score 2185; DB 20; Length 641;
Best Local Similarity 94.1%; Pred. No. 3e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;
QY 1 MSOSTQTNFELSPVFOHIMDFLEOPICSVOPIDLNFDPESEDGATKIEISMCIRMQ 60
DB 1 msgstqtnfslspvfohlmfdeopicsvopidlnfdpegedatnkietismcirmq 60

```
QY 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 120
D 61 dsdlsdpmpqyntnlglnsmdqiqngssstspyntdhaonstvaptspyaqpsftdal 120
QY 121 SPSPAIISNTDYPGPHSFVDFVFOQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVTPP 180
D 121 spspaiisntdypgphsfdfvsfqssstaksatwstelyclkklycqiaktcpdqikvmtpp 180
QY 181 POGAVIRAMPYVYKKAHEVTEVVKRCNHELISREFNEGQIAPPSHLIVEGNSHNOYVEDP 240
D 181 pogaVirampvykkaehvtevkrcpnhelisrefnegiappsnllivegnshaqyvedp 240
QY 241 ITGROSALVPEYEPPOVGEFTTLYLNFMCNSSCVGGMRRPILITVLETRDQVGLGRRC 300
D 241 itgrsavlpyeppqvgefttlylnfmcnsscvggmrrpiliivletrdqvlgrrc 300
QY 301 FEARICACPGDRKADBDSTIRKQOVSDSTKNGDGTAKRPFQNTHGIONTSIKRRSPDDE 360
D 301 fearicacpgrdkadedstirkqvsdskngdgtkrpfqntnhtgiontsikrrspdde 360
QY 361 LLYLTVRGRETYEMLLKIKESLEIMOYLPQHTIETRYROOQOQHLOKHLISACFRNE 420
D 361 llylTVrgretyemllkikesleimoylpqhtletcryrqgqqqnhllqk----- 410
QY 421 LVEPRRETPKQSDVFFRHSKRP 442
D 421 -----qtsiqspssygnsspp 426
```

RESULT 9

AAB11358 standard; Protein: 641 AA.

AAB11358;

21-FEB-2001 (first entry)

Human p63 protein isoform #2.

Lung cancer: therapy; treatment; human; tumor; immunogenic; cytostatic;

vaccine; detection.

Homo sapiens.

MO200061612-A2.

19-OCT-2000.

03-APR-2000; 2000MO-US08896.

02-APR-1999; 9905-0285479.

17-DEC-1999; 9905-0466396.

30-DEC-1999; 9905-0476496.

10-JAN-2000; 2000US-0480884.

22-FEB-2000; 2000US-0510376.

(CORI-) CORIXA CORP.

Wang T, Fan L;

MPI; 2000-628399/60.

N-PDB; AAC66028.

Isolated polypeptide comprising an immunogenic portion of a lung tumor

protein is used for detecting and monitoring progression of lung cancer

in a patient -

Disclosure: Page 245-247; 261pp; English.

CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.

Sequence 641 AA:

Query Match 91.7%; Score 2185; DB 21; Length 641;

Best Local Similarity 94.1%; Pred. No. 3e-189; 7; Indels 16; Gaps 1;

Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

```
QY 1 MSOSTQNEELSPVFEFHIMDFLEQPTICSVQPIDNLNVDEPSEGAATKIEISMDICRMQ 60
D 1 msostqneelspvfevfhimdfleqplicsvqpidnlvdepsedgatnkieleismdicrmq 60
QY 61 DSDLSDPMPQYNTNLGLNSMDQIQNGSSSTSPYNTDHAONSVTAPSPYAQPSTFDAL 120
D 61 dsdlsdpmpqyntnlglnsmdqiqngssstspyntdhaonstvaptspyaqpsftdal 120
QY 121 SPSPAIISNTDYPGPHSFVDFVFOQSSSTAKSATWYSTELKLYCQIAKTCPIQIKVTPP 180
D 121 spspaiisntdypgphsfdfvsfqssstaksatwstelyclkklycqiaktcpdqikvmtpp 180
QY 181 POGAVIRAMPYVYKKAHEVTEVVKRCNHELISREFNEGQIAPPSHLIVEGNSHNOYVEDP 240
D 181 pogaVirampvykkaehvtevkrcpnhelisrefnegiappsnllivegnshaqyvedp 240
QY 241 ITGROSALVPEYEPPOVGEFTTLYLNFMCNSSCVGGMRRPILITVLETRDQVGLGRRC 300
D 241 itgrsavlpyeppqvgefttlylnfmcnsscvggmrrpiliivletrdqvlgrrc 300
QY 301 FEARICACPGDRKADBDSTIRKQOVSDSTKNGDGTAKRPFQNTHGIONTSIKRRSPDDE 360
D 301 fearicacpgrdkadedstirkqvsdskngdgtkrpfqntnhtgiontsikrrspdde 360
QY 361 LLYLTVRGRETYEMLLKIKESLEIMOYLPQHTIETRYROOQOQHLOKHLISACFRNE 420
D 361 llylTVrgretyemllkikesleimoylpqhtletcryrqgqqqnhllqk----- 410
QY 421 LVEPRRETPKQSDVFFRHSKRP 442
D 421 -----qtsiqspssygnsspp 426
```

RESULT 10

AAB11361 standard; Protein: 680 AA.

AAB11361;

21-FEB-2001 (first entry)

Human p63 protein isoform #5.

Lung cancer: therapy; treatment; human; tumor; immunogenic; cytostatic;

vaccine; detection.

Homo sapiens.

MO200061612-A2.

19-OCT-2000.

03-APR-2000; 2000MO-US08896.

02-APR-1999; 9905-0285479.

17-DEC-1999; 9905-0466396.

30-DEC-1999; 9905-0476496.

10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

XX (CORI-) CORIXA CORP.

XX Wang T, Fan L;

XX WPI; 2000-628399/60.

DR N-PSDB; AAC66031.

XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
in a patient -

PS Disclosure: Page 250-253; 261pp; English.

CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4 and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.

XX Sequence 680 AA;

Query Match 91.7%; Score 2185; DB 21; Length 680;
Best Local Similarity 94.1%; Pred. No. 3.3e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNELSPVFOHIMDFLEOPICSVQPIDLNFWDEPSEDGATNKIEISMDICRMQ 60
DB 40 msqstqtnelspvfohimgflefqplcsvqpidlnfvdpsedgatkietismdclmq 99
QY 61 DSDLSDPMPQVYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSSTFDAL 120
DB 100 dsdlsdpmpvynlglinsmdqoiongssstspyntdhaonsvtapspyapqssstfdal 159
QY 121 SPSPALPSNTDYGPSPFVSFOQSSSTAKSATWYSTEILKLYCOIATCPQIQKVMTPP 180
DB 160 spspalpsntdygpshfvsfqsstakstakwylstlkllycqiactpqiqlkvmtp 219
QY 181 PGCAVIRAMPVYKKAHEVTVKRCPNHELREFEFGOIAAPSHIRVGNSHAQYVEDP 240
DB 220 pgcavirampvykkaehvtevkrcpnhelrefefngoiapshirvgnshaqyvedp 279
QY 241 ITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGAMNRRPILIVTLETRDGOVLGRRC 300
DB 280 itgrqsvlypeppqvgtetvlynfmcnsscvgammrrpiliivtletrdgovlgrrc 339
QY 301 FEARICACGRKRADEDSIRKQOVSSTKNGDGTAKRPFRONTGCIOWTSIKRRSPDDE 360
DB 340 fearicacgrkadedsirkgvssstknngdgtakrpfrrontgciowtsikrrspdde 399
QY 361 LLYLVRGRETEYEMLKTESLEMOYLPOHTTETTYRQOQOQOHNLLOKHLISACFRNE 420
DB 400 llylvrgretemlktleslemoylpohthtetyrqooqooqohnllokhlisacfrne 449
QY 421 LYPERRETPKOSDVFRHRSKPP 442
DB 450 -----qtslqspssysgnssp 465

RESULT 11

AAV50997

ID AAV50997 standard; Protein; 680 AA.

AC AAV50997;

XX

DT 14-MAR-2000 (first entry)

XX Human KET protein.

DE KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

KW p53 family; angiogenic; cytotoxic; cancer; human.

XX Homo sapiens.

OS WO9961610-A2.

PN 02-DEC-1999.

XX 25-MAY-1999; 99WO-DE01557.

PF 25-MAY-1999; 98DE-1022985.

XX (FRAU) FRAUNHOFER GES FORDERUNG ANGEWANDTEN.

PA Paul D, Augustin M, Schmale H, Bamberger C;

PI WPI; 2000-062710/05.

DR N-PSDB; AA243913.

XX New KET-encoding nucleic acid and related proteins, for diagnosis and

PT treatment of tumors -

XX Claim 7; Page 26-28; 28pp; German.

CC This invention describes a novel KET-encoding nucleic acid (I) and its
CC fragments, variants and mutants which has anticancer activity. (I)
CC encodes a protein, (II), involved in control of the cell cycle and
CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
CC detect (I) in biological samples, specifically angiogenic tumor tissue,
CC including (I) sequences that have a homozygotic deletion and (b) to
CC detect presence or absence of human chromosome 3q27 or murine chromosome
CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor
CC suppressor, particularly in tumors where an alteration in the wild-type
CC p53 allele has not been identified. (I) and (II) may also be used for
CC development of specific cytotoxic agents and for predicting the risk of
CC development of cancer. This sequence represents the human KET protein
CC described in the method of the invention.

XX Sequence 680 AA;

Query Match 91.7%; Score 2185; DB 21; Length 680;
Best Local Similarity 94.1%; Pred. No. 3.3e-189;
Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSQSTQTNELSPVFOHIMDFLEOPICSVQPIDLNFWDEPSEDGATNKIEISMDICRMQ 60
DB 40 msqstqtnelspvfohimgflefqplcsvqpidlnfvdpsedgatkietismdclmq 99
QY 61 DSDLSDPMPQVYTNLGLNSMDQOIONGSSSTSPYNTDHAONSVTAAPSPYAPQSSSTFDAL 120
DB 100 dsdlsdpmpvynlglinsmdqoiongssstspyntdhaonsvtapspyapqssstfdal 159
QY 121 SPSPALPSNTDYGPSPFVSFOQSSSTAKSATWYSTEILKLYCOIATCPQIQKVMTPP 180
DB 160 spspalpsntdygpshfvsfqsstakstakwylstlkllycqiactpqiqlkvmtp 219
QY 181 PGCAVIRAMPVYKKAHEVTVKRCPNHELREFEFGOIAAPSHIRVGNSHAQYVEDP 240
DB 220 pgcavirampvykkaehvtevkrcpnhelrefefngoiapshirvgnshaqyvedp 279
QY 241 ITGRQSVLYPEPPQVGTETTVLYNFMCNSSCVGAMNRRPILIVTLETRDGOVLGRRC 300
DB 280 itgrqsvlypeppqvgtetvlynfmcnsscvgammrrpiliivtletrdgovlgrrc 339
QY 301 FEARICACGRKRADEDSIRKQOVSSTKNGDGTAKRPFRONTGCIOWTSIKRRSPDDE 360
DB 340 fearicacgrkadedsirkgvssstknngdgtakrpfrrontgciowtsikrrspdde 399

Db 340 fearicacpgrdirkdedsirkqvsdskngdtkrpfirngthngtmslktkrrspdde 399
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLLOKHLILSACFEENE 420
 CC |||||
 CC 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQGGQGHLLQK----- 449
 Db 421 LVEPRRETPKOSDVFFRHSKRP 442
 QY : : : : :
 Db 450 -----qtsiqspssysgnsspp 465

RESULT 12
 AAY05958
 ID AAY05958 standard; Protein; 680 AA.
 XX
 AC AAY05958;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human cell regulatory protein p63, isoform delta p63 gamma.
 XX
 KW Cell regulatory protein; p63; hu-delta p63 gamma; human;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO9919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PF 02-OCT-1998; 98WO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F, Yang A;
 XX
 XX WPI; 1999-277595/23.
 DR N-PSDB; AAX58577.
 XX
 DR New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 23; Fig 14; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents human
 CC p63 isoform hu-delta p63 gamma. p63 was detected in a variety
 CC of human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX58572-83) and anti-p63 antibodies of the invention can be used to

CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC XX
 S0 Sequence 680 AA;

Query Match 91.0%; Score 2169; DB 20; Length 680;
 Best Local Similarity 93.2%; Pred. No. 9,3e-188;
 Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;

QY 1 MSOSTOTNEFLSPVEFQIHMDLEQPTCSYQPIDLNFVDEPSEDGATNKIEISMDCIIMQ 60
 Db |||||
 Db 40 msgstqlseflspvefqlwdflegpicvqplanfvdpsenganklelmsndclmq 99
 QY 61 DSDLSDFPMPOYTNGCLNSMDQOIQNGSSSTSPYNDHAQNSTVAPSAQESTDIAL 120
 Db |||||
 Db 100 dsdlsdpmwpqytnlglinsmdqqlqngssastpyntlhaqnsylvapsyqpsatfda 159
 QY 121 SPSFAIPSENTDYPGPHSFDVSFEQSSSTPAKSATWTYSTFLKLYCOIAKTCPIQIKVMTTP 180
 Db |||||
 Db 160 spspalpsntclpypbhsfdvsfqsstakstwtystelklycqiaktcpqlkwmtp 219
 QY 181 PGAVIRAMPYKKAHEHYEVYKRCPNHELSEFNEGOIAPPSHLIRYEGNSHAQYEDP 240
 Db |||||
 Db 220 pgavirampykkahelvkrpcphelshrefnegqlappshlirvegnshaqyvedp 279
 QY 241 ITGRQSVLYPREPQVQYGFETTVLYXNFMCNSSCYGAMRRPILITVLETDDQVLAGRC 300
 Db |||||
 Db 280 ltgrqsvlyprepvygvtetvlylnfmcnsscvygmrrpiltvletddqvlagrc 339
 QY 301 FEARICACPGRRKRADEDSIRKQOVSSTKNGDGTKRPFRONTGCIOWTSIKRRSPDDE 360
 Db |||||
 Db 340 fearicacpgrdirkdedsirkqvsdskngdtkrpfirngthngtmslktkrrspdde 399
 QY 361 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYROOQOOHOLLOKHLILSACFEENE 420
 Db |||||
 Db 400 LLYLPVGRRETYEMLLKIKESLELMQYLPQHTIETRYRQGGQGHLLQK----- 449
 QY 421 LVEPRRETPKOSDVFFRHSKRP 442
 Db : : : : :
 Db 450 -----qtsmqsgssysgnsspp 465

RESULT 13
 AAY05998
 ID AAY05998 standard; Protein; 680 AA.
 XX
 AC AAY05998;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Rat KET protein.
 XX
 KW KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;
 KW p53 family; angiogenic; cytotoxic; cancer; rat.
 XX
 OS Rattus sp.
 XX
 PN WO9961610-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 25-MAY-1999; 99WO-DE01557.
 XX
 PR 25-MAY-1998; 98DE-1022985.
 XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 PI Paul D, Augustin M, Schmale H, Bamberger C;
 XX
 DR WPI; 2000-062710/05.
 XX

|||||
Db 195 pyppqytleftvlylntmcnscvsgmarrp1llivletrdqvlgrrcfearicacp 254
OY 310 GRDRKADSDSIRKQOVSDSTKNGDGTAKRPFRONTNGIOMTSIKRRSRDDELTYLPVGR 369
Db 255 grdrkadedsirkqvdsstkngdgktrprrngtngtqmsikrrspddellylpvgr 314
OY 370 ETYEMLLKIKESLEIMQYLPQHTIETRYRQOQOQHLLQKHLISACPRNELVEPRRET 429
Db 315 etyemllkikeslelmqylpqhtietryrqgqgqghllqghllsactrnelveprretp 374
OY 430 KQSDVFRHRSKPPNRSYVP 448
Db 375 kgsdvfrhskppnrsvyp 393
RESULT 15
AAV05964
ID AAV05964 standard; protein: 389 AA.
AC AAV05964;
XX
XX
DT 16-AUG-1999 (first entry)
XX
DE Mouse cell regulatory protein p63, isoform delta p63 gamma, CDNA.
XX
KM Cell regulatory protein: p63; mu-delta p63 gamma; mouse:
KM cancer; tumour suppressor; cell cycle control; apoptosis;
KM cell proliferation; cell differentiation; therapy.
XX
OS Mus sp.
XX
PN MO9919357-A2.
XX
PD 22-APR-1999.
XX
XX 02-OCT-1998; 98MO-US21992.
PF
XX 29-MAY-1998; 98US-0087216.
PR 15-OCT-1997; 97US-0062076.
PR
XX (HARD) HARVARD COLLEGE.
PA
XX MKeon F, Yang A;
PI
XX WPI: 1999-277595/23.
DR N-PSDB; AAX58583.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
PS Claim 23: Fig 20: 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
CC RACE. Sequencing of the amplification product indicated that the
CC amplified cDNA possessed a truncated N-terminus, i.e. the
CC transactivation domain was absent. Additional splice variants were
CC identified by screening a cDNA library with a probe corresponding
CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
CC variants differing at the C-terminus are designated as alpha, beta
CC and gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and gamma forms, where the delta form lacks the
CC transactivation domain. The present sequence represents mouse p63
CC isoform mu-delta p63 gamma. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta and gamma
CC act as dominant negatives towards transactivation by p53 and p63.

CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAV05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 389 AA;
Query Match 81.3%; Score 1938; DB 20; Length 389;
Best Local Similarity 97.1%; Pred. No. 3,5e-167;
Matches 368; Conservative 0; Mismatches 7; Indels 4; Gaps 1;
OY 70 PQTNLGLNSMDOOITONGSSSTSPYNTDHAQNSTAPYAQPSFTDALSPPAIPSN 129
Db 15 pytnlglnsmddq1qgssstspyntdhaqnsvtapsyapqstfdalsppalpsn 74
OY 130 TDYGPBHSFDVSFOOSSTAKSATWTSTELKKLYCOIAKTCPIQIKVTPPPGAVIRAM 189
Db 75 tdypgphsfvdsfgsstaksatwtstelkklycqiaktcpidqikvntpppgaviram 134
OY 190 PVYKKAHEVTEVYKRCPNHELREFNEGOIAPPSHLIRVEGNSHAQYVEDITGROSLV 249
Db 135 pyvkkahvtevkrcpnhelrefneqiappshlirvegnshaqyveditgrqslv 194
OY 250 PYPPQVQTEFTTYLYINMCNSCYGGMNRRPILITVLETRDQVLCRRCFEARICAP 309
Db 195 pyppqvqtleftvlylntmcnscvsgmarrp1llivletrdqvlgrrcfearicacp 254
OY 310 GRDRKADSDSIRKQOVSDSTKNGDGTAKRPFRONTNGIOMTSIKRRSRDDELTYLPVGR 369
Db 255 grdrkadedsirkqvdsstkngdgktrprrngtngtqmsikrrspddellylpvgr 310
OY 370 ETYEMLLKIKESLEIMQYLPQHTIETRYRQOQOQHLLQKHLISACPRNELVEPRRET 429
Db 311 etyemllkikeslelmqylpqhtietryrqgqgqghllqghllsactrnelveprretp 370
OY 430 KQSDVFRHRSKPPNRSYVP 448
Db 371 kgsdvfrhskppnrsvyp 389

Search completed: August 8, 2001, 01:35:36
Job time: 4872 sec

Wed Aug 8 08:03:08 2001

us-09-670-568b-1.rag

Page 12

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 00:15:39 ; Search time 57.45 Seconds

(Without alignments)
160,565 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383
Sequence: 1 MSQSTQTEFLSPVFQHTW.....PKQSDVFRHSPKPSVYP 448Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summariesDatabase : Issued_Patents_AA :
1: /cgnl_7/ptodata/1/1aa/5A.COMB.pep.*
2: /cgnl_7/ptodata/1/1aa/5B.COMB.pep.*
3: /cgnl_7/ptodata/1/1aa/6A.COMB.pep.*
4: /cgnl_7/ptodata/1/1aa/6B.COMB.pep.*
5: /cgnl_7/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgnl_7/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	722.5	30.3	393	1 US-08-047-041A-27	Sequence 27, Appl
2	722.5	30.3	393	1 US-08-390-516C-8	Sequence 8, Appl
3	722.5	30.3	393	1 US-08-390-515A-8	Sequence 8, Appl
4	722.5	30.3	393	2 US-08-801-718-8	Sequence 8, Appl
5	717.5	30.1	363	2 US-08-697-221-17	Sequence 17, Appl
6	717.5	30.1	393	1 US-08-047-041A-25	Sequence 25, Appl
7	717.5	30.1	393	1 US-08-047-041A-26	Sequence 26, Appl
8	717.5	30.1	393	1 US-08-347-792-2	Sequence 2, Appl
9	717.5	30.1	393	1 US-08-390-516C-6	Sequence 6, Appl
10	717.5	30.1	393	1 US-08-431-357-2	Sequence 2, Appl
11	717.5	30.1	393	1 US-08-390-515A-6	Sequence 6, Appl
12	717.5	30.1	393	1 US-08-380-515A-7	Sequence 7, Appl
13	717.5	30.1	393	1 US-08-380-515A-7	Sequence 7, Appl
14	717.5	30.1	393	2 US-08-795-006A-32	Sequence 32, Appl
15	717.5	30.1	393	2 US-08-697-221-2	Sequence 2, Appl
16	717.5	30.1	393	2 US-08-801-718-6	Sequence 6, Appl
17	717.5	30.1	393	2 US-08-801-718-7	Sequence 7, Appl
18	717.5	30.1	393	2 US-08-247-904B-12	Sequence 12, Appl
19	717.5	30.1	393	3 US-08-767-842A-23	Sequence 23, Appl
20	717.5	30.1	393	4 US-08-352-542-2	Sequence 2, Appl
21	717.5	30.1	393	4 US-09-184-073-32	Sequence 32, Appl
22	717.5	30.1	393	4 US-08-328-673A-9	Sequence 9, Appl
23	717.5	30.1	393	4 US-08-894-327-2	Sequence 2, Appl
24	717.5	30.1	439	5 PCT-US95-15353-2	Sequence 2, Appl
25	717.5	30.1	439	2 US-08-959-638-9	Sequence 9, Appl
26	716.5	30.1	363	1 US-08-697-221-18	Sequence 18, Appl
27	716.5	30.1	393	1 US-08-047-041A-28	Sequence 28, Appl

28	716.5	30.1	393	1 US-08-390-516C-9	Sequence 9, Appl
29	716.5	30.1	393	1 US-08-390-515A-9	Sequence 9, Appl
30	716.5	30.1	393	2 US-08-697-221-3	Sequence 4, Appl
31	716.5	30.1	393	2 US-08-697-221-4	Sequence 9, Appl
32	716.5	30.1	393	2 US-08-801-718-9	Sequence 1, Appl
33	716.5	30.1	393	2 US-08-675-631-1	Sequence 19, Appl
34	713.5	29.9	363	2 US-08-697-221-19	Sequence 11, Appl
35	713.5	29.9	393	2 US-08-697-221-11	Sequence 20, Appl
36	712.5	29.9	363	2 US-08-697-221-20	Sequence 12, Appl
37	712.5	29.9	363	2 US-08-697-221-21	Sequence 14, Appl
38	712.5	29.9	393	2 US-08-697-221-12	Sequence 25, Appl
39	712.5	29.9	393	2 US-08-697-221-14	Sequence 22, Appl
40	712.5	29.9	393	2 US-08-697-221-25	Sequence 15, Appl
41	711.5	29.9	363	2 US-08-697-221-22	Sequence 27, Appl
42	711.5	29.9	393	2 US-08-697-221-15	Sequence 15, Appl
43	711.5	29.9	393	2 US-08-697-221-27	Sequence 15, Appl
44	711	29.8	390	1 US-08-347-792-15	Sequence 15, Appl
45	711	29.8	390	1 US-08-431-357-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-047-041A-27
Sequence 27, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047, 041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928, 661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446, 584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330, 566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 AUTHORS: Harris, et al.,
 JOURNAL: Mol. Cell. Biol.
 VOLUME: 6
 ISSUE: 12
 PAGES: 4650-4656
 DATE: 1986
 US-08-047-041A-27

Query Match 30.3%; Score 722.5; DB 1; Length 393;
 Best Local Similarity 40.5%; Pred. No. 1.2e-60;
 Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPEVFOHIMDFEOPICVQPIDLNFVDEPSEEDGATNKIEISMDICIMODSDLSDEMPMP 70
 DB 14 LSQETFSDLKLLPE-----NNVLSPLPSQAMDDMLSPDDIEQWTE--DP--- 58
 QY 71 QYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYQSPSTFALSPPSA----- 125
 DB 59 -----GPDAPRMEAPPAVAPATPTPPAPAPAPASWPL 93
 QY 126 ---IPSNTRYDGPSPHSDVFSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQ 182
 DB 94 SSSVPSQKTYGSGYGFRLGFLHSGTAKSVCTYSPALNKKMFCQIAKTCPIQIAKTCPIQIKWTPPPQ 153
 QY 183 GAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGCNSHAQYVEDPIT 242
 DB 154 GTRVRAMAIYKOSQHMTEVVRCPHNE--RCSDSGLAPQHLIRVGCNLRYEYLDDBNT 211
 QY 243 GROSVLVPEPPOVGTETTYLVNFMCNSSCGVMNRPLIILVLETRDGOVLGRCFE 302
 DB 212 FRHSVVPYEPPEVSGDCTTIHYNYMCNSSCGVMNRPLIITITLEDSSGNLGRNSE 271
 QY 303 ARICACPRDKADEDSIRKQVSDSTKNGDGTKRPRONTGHIQWTSIKRRSP--DDEL 361
 DB 272 VRVACPCGRDRTEEMLRKGPBHHELPGSTKRALPNT-----SSSPQPKKKPLDGEY 327
 QY 362 LYLPRGRETEYEMLKIKESLEL 384
 DB 328 FTLOIRGRETEYEMFRELNEALEL 350

RESULT 2
 US-08-390-516C-8
 Sequence 8, Application US/08390516C
 Patent No. 5708136
 GENERAL INFORMATION:
 APPLICANT: BURRELL, MARILEE
 APPLICANT: HILL, DAVID E.
 APPLICANT: KINZLER, KENNETH W.
 APPLICANT: VOGELSTEIN, BERT
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G STREET, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,516C

FILING DATE: 07-APR-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107,42798
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BMBB UR
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 AUTHORS: Harris, et al.,
 JOURNAL: Mol. Cell. Biol.
 VOLUME: 6
 ISSUE: 12
 PAGES: 4650-4656
 DATE: 1986
 US-08-390-516C-8

Query Match 30.3%; Score 722.5; DB 1; Length 393;
 Best Local Similarity 40.5%; Pred. No. 1.2e-60;
 Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPEVFOHIMDFEOPICVQPIDLNFVDEPSEEDGATNKIEISMDICIMODSDLSDEMPMP 70
 DB 14 LSQETFSDLKLLPE-----NNVLSPLPSQAMDDMLSPDDIEQWTE--DP--- 58
 QY 71 QYTNGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPYQSPSTFALSPPSA----- 125
 DB 59 -----GPDAPRMEAPPAVAPATPTPPAPAPAPASWPL 93
 QY 126 ---IPSNTRYDGPSPHSDVFSFOOSSTAKSATWTYSTELKLYCQIAKTCPIQIKWTPPPQ 182
 DB 94 SSSVPSQKTYGSGYGFRLGFLHSGTAKSVCTYSPALNKKMFCQIAKTCPIQIAKTCPIQIKWTPPPQ 153
 QY 183 GAVIRAMPYKKAHVTEVVKRCPNHLSREFNEGQIAPPSHLIRVGCNSHAQYVEDPIT 242
 DB 154 GTRVRAMAIYKOSQHMTEVVRCPHNE--RCSDSGLAPQHLIRVGCNLRYEYLDDBNT 211
 QY 243 GROSVLVPEPPOVGTETTYLVNFMCNSSCGVMNRPLIILVLETRDGOVLGRCFE 302
 DB 212 FRHSVVPYEPPEVSGDCTTIHYNYMCNSSCGVMNRPLIITITLEDSSGNLGRNSE 271
 QY 303 ARICACPRDKADEDSIRKQVSDSTKNGDGTKRPRONTGHIQWTSIKRRSP--DDEL 361
 DB 272 VRVACPCGRDRTEEMLRKGPBHHELPGSTKRALPNT-----SSSPQPKKKPLDGEY 327
 QY 362 LYLPRGRETEYEMLKIKESLEL 384
 DB 328 FTLOIRGRETEYEMFRELNEALEL 350

RESULT 3
 US-08-390-515A-8
 Sequence 8, Application US/08390515A
 Patent No. 5756455
 GENERAL INFORMATION:
 APPLICANT: BURRELL, MARILEE
 APPLICANT: HILL, DAVID E.
 APPLICANT: KINZLER, KENNETH W.
 APPLICANT: VOGELSTEIN, BERT
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/390,515A
FILING DATE: 07-APR-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Harris, et al.,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-390-515A-8

Query Match 30.3%; Score 722.5; DB 1; Length 393;
Best Local Similarity 40.5%; Pred. No. 1.2e-60;
Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPFVFOHIDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDCTRMODSDLSDPMP 70
DB 14 LSOETFSIDLKILPE-----NNVLSPLPSQAMDILMSDDIEQWTE--DP--- 58
QY 71 QYTNLGLINSMDQIQNGSSSTSPYNTDHAONSYTAPSPYAQPSSTFDALSPSPA----- 125
DB 59 -----GPDAPRPMPEAPPVAPAPATPTPAAPAPAPSPML 93
QY 126 ---IPSTNDYRGHSPDVNSFOQSTASTATYTYSTELKLYCQIAKCPIDQIKMTTPPQ 182
DB 94 SSSVPSQKTYQSGTFLGHSCTAKSVCTYSPALNKMFCQIAKCPYQWLWDSSTPP 153
QY 183 GAVIRAPVYKKAHEVYKRCPNHLSREFNCGOIAPSHILRVGNSHAQVVEPIT 242
DB 154 GTRVRAAIIKQSOHMEVYKRCPHNE--RCSDSGLAPQOHLIRVGNLRVEYLDNRNT 211
QY 243 GROSIVLPEPPOVGETTEVLYNFMCNSSCVGGMNRRPILITLTETRDGOVLRGCFE 302
DB 212 FRHSVYVPEPEVGSCTIITHYKMCSSCMGMNRRPILITITLDDSGNLLGRSFE 271
QY 303 ARICACGRKAKADESIRKQOVSSTKNGDGTKRPRONTHTGIQTSIKKRSP-DDEL 361
DB 272 VRVACGGRDRKTEENLRKKGEPRHMLPGSTKRALPNNT---SSSPQPKKKPLDGEY 327

QY 362 LYLPVGRRETYEMLKIKESLEL 384
DB 328 FTLQIRGREREREMLELEALEL 350

RESULT 4
US-08-801-718-8
Sequence 8, Application US/08801718
Patent No. 5858976
GENERAL INFORMATION:
APPLICANT: BURRELL, MARILEE
APPLICANT: HILL, DAVID E.
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
TITLE OF INVENTION: HUMAN TUMORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Harris, et al.,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-801-718-8

Query Match 30.3%; Score 722.5; DB 2; Length 393;
Best Local Similarity 40.5%; Pred. No. 1.2e-60;
Matches 155; Conservative 57; Mismatches 116; Indels 55; Gaps 7;

QY 11 LSPFVFOHIDFLEOPICSVQPIDLNFVDEPSEDGATNKIEISMDCTRMODSDLSDPMP 70
DB 14 LSOETFSIDLKILPE-----NNVLSPLPSQAMDILMSDDIEQWTE--DP--- 58

Db 332 IRGRERFEMFELNEALEL 350

RESULT 8

US-08-347-792-2

Sequence 2, Application US/08347792

Patent No. 5573925

GENERAL INFORMATION:

APPLICANT: Halazonetis, Thanos D.

TITLE OF INVENTION: p53 Proteins With Altered

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,792

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST580USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-5818

TELEFAX: 215-540-9206

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-347-792-2

Query Match 30.1%; Score 717.5; DB 1; Length 393;

Best Local Similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

11 LSPEVFOHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56

14 LSOETFSIDLMLKLPENNVLSPQAMDMLSPDDIQWFTEDPGPDEA----- 63

57 IRMODSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPST 116

64 -----PRMPE-----APP-----VAPAP-AAFTPA 83

117 FDALSP-----SPALPSNDYDGPSPHSDVVSFOOSSTANSATWTYSTELKLYCOIAKTCP 172

84 APAPAPSPPLSSVPSQKTTGGSTGFRGLHSGTAKSVCTYSPALNKMFCOLAKTCPV 143

173 QIKVMTPEPGAVIRAMPVYKKAHEVTVKRCPNHFLSREFNNGOIAAPSHLIRVCGNS 232

144 QLVWDSPRPPTGTRVRAIMATIKQSQHMTVEVRRCPHNE--KCSSDGLAPQOHLIRVEGNL 201

233 HAQVDEPPIGRGSLVLYPERPOVGETFTVLYVFCMNCSSCVGMMNRPIILITVLETRD 292

202 RVEVLDRNFRHSVYVPEPEVSGDCTIHYNYMNCSSCMGMNRRPILITITLEDSS 261

293 GVLGRGCFARICACGPRGRKADIEDIRKOQVSDSTKNGDGKKRFRQTHGIQMTSIK 352

262 GNLLGRNSFEVRVACGCRGRDRTTEENLRKKGEPHHELPGSTKRALPNNT-----SSSPD 317

QY 353 KRSP-DDELLYLPYGRREYEMLKIKESIEL 384

Db 318 PKKKPLDGEYFTLQIRGRERFEMFELNEALEL 350

RESULT 9

US-08-390-516C-6

Sequence 6, Application US/08390516C

Patent No. 5708136

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,516C

FILING DATE: 07-Apr-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107,42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOPHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

AUTHORS: Buchanan, et al.,

JOURNAL: Gene

VOLUME: 70

PAGES: 245-252

DATE: 1988

US-08-390-516C-6

Query Match 30.1%; Score 717.5; DB 1; Length 393;

Best Local Similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

11 LSPEVFOHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56

14 LSOETFSIDLMLKLPENNVLSPQAMDMLSPDDIQWFTEDPGPDEA----- 63

57 IRMODSDLSDPMPQYTNLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPSPST 116

64 -----PRMPE-----APP-----VAPAP-AAFTPA 83

117 FDALSP-----SPALPSNDYDGPSPHSDVVSFOOSSTANSATWTYSTELKLYCOIAKTCP 172

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Db 84 AAPAPSPMLSSSVPSQKTVQGSYGFRGLGHSSTAKSVCTCTSPALNKKMFQCLAKTCPV 143
QY 173 QIKVMTPPGCAVIRAMPYKKAEHVTYVKRCPNHLSFENEGQIAPPSHLIRVGCNS 232
Db 144 ILWVDSPPPGTRRAVMAIKOSQHMTEVVRCPNHE--RCSDSDGLAPPOHLIRVGCNL 201
QY 233 HAQVDEPITGRSVLPVYPPPOVGTFTVLVNFMCNSSCGVGMNRRPILITVLETRD 292
Db 202 RVEYLDNRNFRHSVYVYPPPEVGSCTTIHYNMCNSSCGMGNRRPILITILEDDS 261
QY 293 GOVYLRRCFEARICACGRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIK 352
Db 262 GNILGRNFEVRCACGRDRTEENLRKKGEPRHHLPGSTKRALPNNT----SSSPQ 317
QY 353 KRKSP-DELLIYPRGRETYEMLIKESLEL 384
Db 318 PKKKPLDGEYFTLIQIRGREREMRELNEALEL 350

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RESULT 10
US-08-390-516C-7
; Sequence 7, Application US/08390516C
; Patent No. 5708136
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/390,516C
; FILING DATE: 07-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: KAGAN, SARAH A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 01107.42798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 197430 BBMB UT
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Harris, et al.,
; JOURNAL: Mol. Cell. Biol.
; VOLUME: 6
; ISSUE: 12
; PAGES: 4650-4656
; DATE: 1986

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US-08-390-516C-7

Query Match 30.18; Score 717.5; DB 1; Length 393;
 Best Local Similarity 41.28; Pred. No. 3.5e-60;
 Matches 156; Conservative 60; Mismatches 116; Indels 47; Gaps 9;

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QY 11 LSPVEFHINDLEOPICSVQPIDLNFVDEPSEDGATNKIKESIMDCIRMDSDLSDMWP 70
Db 14 LSOFTFSDMLKLP-----NNVLSPLPSQAMDMLSPDIEQWFT--DP--- 58
QY 71 QYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSAOPSSTFDALSP---SPA 126
Db 59 -----GPDEAPRMEAPR--VAAP-ATPPAPAPAPSPMLSSSV 97
QY 127 PSNTDYGPHSPFVSPQOOSTAKSATWITSTELKKLYCQIAKTCPIQIKMTPPGCAV 186
Db 98 PSQRTYQGSYGRGLGFLHSSTAKSVCTCTSPALNKKMFQCLAKTCPVOLWVDSPPGTRV 157
QY 187 RAMPYKKAHVTYVKRCPNHLSREFNEGQIAPPSHLIRVEGNSHAQVDEPITGRS 246
Db 158 RAMATYKQSOHMTVEVRCPNHE--RCSDSDGLAPPOHLIRVGSNLVETLDNRTRHS 215
QY 247 VLVEPPPOVGTFTFTVLVNFMCNSSCGVGMNRRPILITVLETRDGOVLRRCFEARIC 306
Db 216 VVVPPEPPVGSCTTIHYNMCNSSCGMGNRRPILITILEDSGNLGRNFEVRC 275
QY 307 ACPGRDRKADEDSIRKQOVSSTKNGDGTKRPRONTGHIOMTSIKKRSP-DELLIYLP 365
Db 276 ACPGRDRTEENLRKKGEPRHHLPGSTKRALPNNT----SSSPQKKRPLDGEYFTLIQ 331
QY 366 VGRGRETYEMLIKESLEL 384
Db 332 IRGREREMRELNEALEL 350

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RESULT 11
US-08-431-357-2
; Sequence 2, Application US/08431357
; Patent No. 5721340
; GENERAL INFORMATION:
; APPLICANT: Halazonetis, Thanos D.
; TITLE OF INVENTION: p53 Proteins with Altered
; TITLE OF INVENTION: Tetramerization Domains
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., PO Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,357
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/347,792
; FILING DATE: 28-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST58USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-5818
; TELEFAX: 215-540-9206
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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LENGTH: 393 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-431-357-2

Query Match 30.1%; Score 717.5; DB 1; Length 393;
 Best Local Similarity 39.7%; Pred. No. 3,5e-60;
 Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPEVFGHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56
 DB 14 LSGFTFSLDKLLPENNVLSPFQAMDMLSPDDIEQWTFEDPDPDEA----- 63
 QY 57 IRMODSLDPMMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTPAPSPYAPSSST 116
 DB 64 -----PRMPE-----AAP-----VAPAP-AAPIPA 83
 QY 117 FDALSP-----SPAIPSTNDYPGPHSPDVSFQOOSTAKSATWTSTELKLYCOIAKTCPI 172
 DB 84 APAPAPSMPLSSSVSPQKTYGSGYGRGLGHSHTAKSVCTCTSPALNKMFCQIAKTCPIV 143
 QY 173 QIKYMPPPGAVIRAMPYVKAHEVTEVYKRCPNHLSREFNEGQIAPPSHLIRVEGNS 232
 DB 144 QLVWDSIPPEGTRVRAVMAIKQSOHMEVYRCPHNE--RCSDSGLAPPOHLIRVEGNL 201
 QY 233 HAQVEDPITGRQSVLVPEYPPQVTEFTTVLYNFMCNSSCVGGMRRPILITVLETRD 292
 DB 202 RVEYLDNRFTFRISVYVPEYEPVGSDCCTTHYNMCSNGCMGMRPILITVLETRDSS 261
 QY 293 GOVLGRCEARICACPGDRKADSDIRKQVSDTKNGDGTGRPRFRONTNGIOMTSIK 352
 DB 262 GNILGRNFEVRCACPGDRRTREENLRKGEHPHELPGSTKRALPNNT-----SSSPQ 317
 QY 353 KRSP--DDELLYLPVGRRETEMLKIKESLEL 384
 DB 318 PKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

RESULT 12

US-08-390-515A-6
 Sequence 6, Application US/08390515A
 Patent No. 5756455

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE
 APPLICANT: HILL, DAVID E.
 APPLICANT: KINZLER, KENNETH W.
 APPLICANT: VOGELSTEIN, BERT
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G STREET, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,515A
 FILING DATE: 07-APR-1993
 CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.42798
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BMB UT
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 PUBLICATON INFORMATION:
 AUTHORS: Buchanan, et al.,
 JOURNAL: Gene
 VOLUME: 70
 PAGES: 245-252
 DATE: 1988
 US-08-390-515A-6

Query Match 30.1%; Score 717.5; DB 1; Length 393;
 Best Local Similarity 39.7%; Pred. No. 3,5e-60;
 Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPEVFGHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSEDGATNKIEISMDC 56
 DB 14 LSGFTFSLDKLLPENNVLSPFQAMDMLSPDDIEQWTFEDPDPDEA----- 63
 QY 57 IRMODSLDPMMPQYTNGLNSMDQIQNGSSSTSPYNTDHAQNSVTPAPSPYAPSSST 116
 DB 64 -----PRMPE-----AAP-----VAPAP-AAPIPA 83
 QY 117 FDALSP-----SPAIPSTNDYPGPHSPDVSFQOOSTAKSATWTSTELKLYCOIAKTCPI 172
 DB 84 APAPAPSMPLSSSVSPQKTYGSGYGRGLGHSHTAKSVCTCTSPALNKMFCQIAKTCPIV 143
 QY 173 QIKYMPPPGAVIRAMPYVKAHEVTEVYKRCPNHLSREFNEGQIAPPSHLIRVEGNS 232
 DB 144 QLVWDSIPPEGTRVRAVMAIKQSOHMEVYRCPHNE--RCSDSGLAPPOHLIRVEGNL 201
 QY 233 HAQVEDPITGRQSVLVPEYPPQVTEFTTVLYNFMCNSSCVGGMRRPILITVLETRD 292
 DB 202 RVEYLDNRFTFRISVYVPEYEPVGSDCCTTHYNMCSNGCMGMRPILITVLETRDSS 261
 QY 293 GOVLGRCEARICACPGDRKADSDIRKQVSDTKNGDGTGRPRFRONTNGIOMTSIK 352
 DB 262 GNILGRNFEVRCACPGDRRTREENLRKGEHPHELPGSTKRALPNNT-----SSSPQ 317
 QY 353 KRSP--DDELLYLPVGRRETEMLKIKESLEL 384
 DB 318 PKKPLDGEYFTLQIRGRERFEMFRELNEALEL 350

RESULT 13

US-08-390-515A-7
 Sequence 7, Application US/08390515A
 Patent No. 5756455

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE
 APPLICANT: HILL, DAVID E.
 APPLICANT: KINZLER, KENNETH W.
 APPLICANT: VOGELSTEIN, BERT
 TITLE OF INVENTION: AMPLIFICATION OF HUMAN MD2 GENE IN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G STREET, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA

```

1      ZIP: 20001
2
3      COMPUTER READABLE FORM:
4
5      MEDIUM TYPE: Floppy disk
6
7      COMPUTER: IBM PC compatible
8
9      OPERATING SYSTEM: PC-DOS/MS-DOS
10
11     SOFTWARE: Patentin Release #1.0, Version #1.25
12
13     CURRENT APPLICATION DATA:
14
15     APPLICATION NUMBER: US/08/390,515A
16
17     FILING DATE: 07-APR-1993
18
19     CLASSIFICATION: 514
20
21     ATTORNEY/AGENT INFORMATION:
22
23     NAME: KAGAN, SARAH A.
24
25     REGISTRATION NUMBER: 32,141
26
27     REFERENCE/DOCKET NUMBER: 01107.42798
28
29     TELECOMMUNICATION INFORMATION:
30
31     TELEPHONE: 202-508-9100
32
33     TELEFAX: 202-508-9299
34
35     TELEX: 197430 BBMB UT
36
37     INFORMATION FOR SEQ ID NO: 7:
38
39     SEQUENCE CHARACTERISTICS:
40
41     LENGTH: 393 amino acids
42
43     TYPE: amino acid
44
45     TOPOLOGY: linear
46
47     MOLECULE TYPE: protein
48
49     HYPOTHETICAL: YES
50
51     ANTI-SENSE: NO
52
53     ORIGINAL SOURCE:
54
55     ORGANISM: Homo sapiens
56
57     PUBLICATION INFORMATION:
58
59     AUTHORS: Harris, et al.
60
61     JOURNAL: Mol. Cell. Biol.
62
63     VOLUME: 6
64
65     ISSUE: 12
66
67     PAGES: 4650-4656
68
69     DATE: 1986
70
71     US-08-390-515A-7

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Db 318 PKKKPLDGEYFTLQIRGRERFEREMFRELNALEL 350

RESULT 15

US-08-697-221-2
Sequence 2, Application US/08697221
Patent No. 5847083

GENERAL INFORMATION:

APPLICANT: Halazonetis, Phanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,221
FILING DATE:
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:

NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST64AUSA
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 393 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-697-221-2

Query Match 30.1%; Score 717.5; DB 2; Length 393;
Best local similarity 39.7%; Pred. No. 3.5e-60;

Matches 156; Conservative 60; Mismatches 102; Indels 75; Gaps 11;

QY 11 LSPDEVFOHIMDFLEQ-----PICS-----VOPIDLN--FVDEPSFEDGATNKIEISMDC 56
Db 14 LQETTESDLMKLLPENNVNLSPLPSQAMDDLMLSPDDIEQWTFTEDEPGDEA----- 63
QY 57 IMQSDSLSDPMWPOYTLGLNSMDQOIONGSSSTSPYNTDHAQNSVTAPSPYAPQPSST 116
Db 64 -----PRMPE-----AAP-----VAPAP-AAPTPA 83
QY 117 FDAISP-----SPAIPSNIDYPGPHSPFVSFOQSSSTAKSATWTYSTELKKLYCOIAKTCPI 172
Db 84 APAPAPSPWISSVSQKTYGSGYFRLGLHSGTAKSVTCTTSPALNKMFCOLAKTCPIV 143
QY 173 QIKVTFPPGAGVTRAMPVYKKAHEVTEVVKRCPNHLSREFNEQIAPPSHILIRVEGNS 232
Db 144 QLWVDSITPPECTRKRAVATIKOSQHMTVEVRCRPHNE--RCSDSGLAPQHLIRVEGNTL 201
QY 233 HAQYVEDPTGROSVLVPEPPQVTEFTTLYNFMCNSSCVGGMRRPILITIVLETRD 292
Db 202 RVEYLDNRNTFRHSVYVPEPEVSGDCTTIHNYMKNSSCMGMNRRPILITITLEDSS 261
QY 293 GOYLGRCFCFARICACGRKRADEDSIRKQOVSSTKNGDGTKRPFRONTHGIONTSIK 352

Db 262 GNLLGRNSFEVRYCACPGDRKRTKEENLKKKGPHHELPGSGSTRKALPNNNT-----SSSPQ 317
QY 353 KRSP-DDELLYLPVGRRETYEMLLKIKESLEL 384
Db 318 PKKKPLDGEYFTLQIRGRERFEREMFRELNALEL 350

Search completed: August 8, 2001, 01:36:44
Job time: 4865 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 8, 2001, 00:20:14 : Search time 51.46 seconds
(without alignments)
663.160 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383

Sequence: 1 MSQSTQINEFLSPEVFOHIM.....PKQSDVFFRHSKPNRSYYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR-68:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	847.5	35.6	396	1 JH0631	cellular tumor ant
2	777.5	36.6	363	1 A29376	cellular tumor ant
3	764.5	32.1	367	1 S02193	cellular tumor ant
4	741.5	31.1	386	1 S51648	cellular tumor ant
5	732	30.7	391	1 S02192	cellular tumor ant
6	719.5	30.2	396	1 JH0633	cellular tumor ant
7	717.5	30.1	393	1 DNH053	cellular tumor ant
8	715	30.0	390	1 DNMS53	cellular tumor ant
9	714.5	30.0	393	1 S06594	cellular tumor ant
10	704	29.5	393	2 JC6176	tumor suppressor p
11	702	29.5	381	2 S38824	cellular tumor ant
12	699.5	29.4	391	2 JC6193	tumor suppressor p
13	259.5	10.9	77	2 T46226	cellular tumor ant
14	114.5	4.8	3942	2 T42730	cellular tumor ant
15	111.5	4.7	1819	2 T32008	hypothetical prote
16	110.5	4.6	2529	2 A56923	transcription fact
17	110	4.6	5762	2 A41819	proline-rich pepi
18	109	4.6	4273	2 C69679	polyketide synthas
19	108.5	4.6	701	1 S33709	DHR39-short protei
20	108	4.6	808	1 S33708	nuclear steroid/th
21	107	4.5	1681	1 D54689	protein-tyrosine-p
22	107	4.5	1894	2 C54689	protein-tyrosine-p
23	107	4.5	1912	2 A56178	protein-tyrosine-p
24	106.5	4.5	631	2 T31782	hypothetical prote
25	106.5	4.5	2578	2 A54922	transcription fact
26	105.5	4.4	395	2 A54949	synedcan precursor
27	105	4.4	384	2 T49528	hypothetical prote
28	105	4.4	766	1 S61694	floculation suppr
29	105	4.4	909	2 T06635	hypothetical prote

30	104.5	4.4	1703	2 S15047	SNF2 protein - yea
31	104	4.4	1456	2 T01397	LTR gag/pol polypr
32	103	4.3	1533	2 T00344	hypothetical prote
33	102.5	4.3	780	2 A48143	HF-1 regulatory el
34	102.5	4.3	1203	2 T17415	mycelial surface a
35	102	4.3	628	2 S19150	hypothetical prote
36	100.5	4.2	1505	2 JC4851	hypoxia-inducible
37	100	4.2	600	2 T24447	hypothetical prote
38	99.5	4.2	526	2 T51372	hypothetical prote
39	99.5	4.2	1165	2 S27609	gtpase-activating
40	99.5	4.2	2359	2 T03094	A-kinase anchor pr
41	99.5	4.2	3938	2 T42761	Bassoon protein -
42	99	4.2	15264	2 T15264	hypothetical prote
43	99	4.2	1888	2 T14273	zinc finger protei
44	98.5	4.1	515	2 T40021	hypothetical prote
45	98	4.1	1213	2 A58198	serine/proline-ric

ALIGNMENTS

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RESULT 1
JH0631
cellular tumor antigen p53 - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JH0631
R:de Fromental, C.C.; Pakdel, F.; Chapus, A.; Baney, C.; May, P.; Soussi, T.
Gene 112, 241-245, 1992
A:Title: Rainbow trout p53: cDNA cloning and biochemical characterization.
A:Reference number: JH0631; MUID:92210006
A:Accession: JH0631
A:Molecule type: mRNA
A:Residues: 1-396 <DEF>
A:Cross-References: GB:M75145; NID:9213828; PIDN:AAA49605.1; PID:9213829
A:Experimental source: Liver
A:Comment: This protein is the product of a tumor suppressor gene, p53, whose inactive
C:Superfamily: cellular tumor antigen p53
C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; pho
F:164,167,227,231/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
F:395/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 35.6%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 66-58;
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

QY 11 LSPVFOHIMDFLEQPICSVQPIDLNFVDEPSEEDGATNKIEISMDICRMQDSDLSDPMP 70
    |||||:|
Db 12 LSGSFEDLW-----KMNLEVAVQPPETE---SWV 39

QY 71 QYTLGLINSMDQIQNGSSSTPRYNTDHAQNSVTAPSPVQPS-STPDALS-RSPALPS 128
    |||||:|
Db 40 GYDNF---MMEAPLQ-----VEPDPSLFEVSAEPAPQPSITSLDNGSPPTSVPT 87

QY 129 NTDPGPHSPFVSFOQSTAKSATMTYSTEKLKLYCIAKCPQIOWMPPPGAVIRA 188
    |||||:|
Db 88 TSDIPGALGFOLRFLOSSTAKSVTCITSPDLNKLFCQIAKCPQIOWMPPPGAVIRA 147

QY 189 MPVYKKAHEVTEVVKRPNHSLREFNQGQIAPSHLIRVGNSHAQYVEDPITGRSVL 248
    |||||:|
Db 148 LAIKKTLSDVADVVRKCRPHQSTSENNEGP-APRGHLVAVRGNGRSEYMEGNTLRHSVL 206

QY 249 VPYEPVQVTEFTTVLYNFMQNSCVGGMNRPILITVTLETDRGQVLRRCFAPRIAC 308
    |||||:|
Db 207 VPYEPVQVSECTTVLYNFMQNSCGMNRPIITITLETGOLGRSEFEVRCAC 266

QY 309 PGRRKADDEDSIRKQO---VSDSTFKNGDGTGRKRPQO-NTHGICWTSSTKKRS---PDDE 360
    |||||:|
Db 267 PGRRKTEELNKKQOETTLETKTTPAQGIKRAMKESLAPAPGASKKTSKSPAVSDDE 326

QY 361 LLYLPVGRGTEYEMLLIKESLEIMQVLPQHTTETTYRQO 399
    |||||:|
```

Db 327 IYTLQIRGKREYEMLKRFNDSLESLVPAVDADKYRK 365

RESULT 2

A29376

cellular tumor antigen p53 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A29376; S61531; S72313; I51639

R:Sousssi, T.; de Fromental, C.C.; Mechali, M.; May, P.; Kress, M.

Oncogene 1, 71-78, 1987

A:Title: Cloning and characterization of a cDNA from Xenopus laevis coding for a protein

A:Reference number: A29376; MUID:88143684

A:Accession: A29376

A:Molecule type: mRNA

A:Residues: 1-363 <SOU>

A:Cross-references: EMBL:X05191; NID:964961; PIDN:CAA28821.1; PID:964962

R:Hoever, M.; Clement, J.H.; Wedlich, D.; Montenarh, M.; Knoechel, W.

Oncogene 9, 109-120, 1994

A:Title: Overexpression of wild-type p53 interferes with normal development in Xenopus

A:Reference number: I51639; MUID:94134403

A:Accession: S61531

A:Molecule type: mRNA

A:Residues: 1-293,295-363 <HO>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

R:Hoever, M.; Clement, J.; Wedlich, D.; Montenarh, M.; Knoechel, W.

submitted to the EMBL Data Library, March 1994

A:Reference number: S72313

A:Molecule type: mRNA

A:Residues: 1-51, 'S', 53-70, 72-293, 295-363 <HO>

A:Cross-references: EMBL:X77546; NID:9468513; PIDN:CAA54672.1; PID:9468514

C:Gene: p53

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; phospho

F;362/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.6% Score 777.5; DB 1; Length 363;

Best Local Similarity 42.5% Pred. No. 1.4e-52;

Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

Db 2 SOSTQNEFLSEPVQHTWDFLEQPI-----CSVQPIIDNFVDEPSEDGATKRIEISMDCI 57

Db 4 SSETGMDPLSOTEFEDLSILPLDPLQTVTCRLDLS- EFDYF-----LAADMT 52

Qy 58 RMQDSDLSPMPQYTNGLNSMQOIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSPSTF 117

Db 53 VLOE-----GLMGN-----AVPTVT- 67

Qy 118 DALSPSPALPSTNDTPGPHSFVDSFOQSTAKSATWTYSTELKLYCOIAKTCGIQAKM 177

Db 68 -----SCAVPSTDYAGKYGILQDFQNGTAKSYTCYISPLNKLFCOLAKTCPLAVRVE 122

Qy 178 TPPOGAVIRAMPYKKAHEHTEVYKRCPNHLSREFNEGOIAPPSHLIVEGNSHAQYV 237

Db 123 SPPPGSLIRATAYKAKSEHVAEYKRCPIHRSERVEPGE-DAAPSHLMVEGNLQAYTM 181

Qy 238 EDPTTGROSLVPEYPPQVGTFTVLYNFCNSCGVGNRRPILITVLETRDQVUG 297

Db 182 EDVNSGRHSVCVPEEGPOVGTCTVLYNFCNSCGVGNRRPILITVLETRDQVUG 297

Qy 298 RRCPEARLACPGDRKADSDS-IRKQVSDSTKNGDGTKRPRQNTM--GIOMTSIKR 354

Db 242 RRCPEVAVCACPGDRDRTEDNTKRGKLRPSGK-----RELAAHPSSSEPLPKKR 292

Qy 355 R---SPDELLYLPVRGRETYEMLKKESTELMOYLPOHTI 393

Db 293 LVVVDDEELFTRIKGRSRYEMIKKLNDALDELQESLDOOKV 334

RESULT 3

S02193

cellular tumor antigen p53 - chicken

N:Alternate names: nuclear oncoprotein p53

C:Species: Gallus gallus (chicken)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S02193

R:Sousssi, T.; Beque, A.; Kress, M.; Stehelin, D.; May, P.

Nucleic Acids Res. 16, 11383, 1988

A:Title: Nucleotide sequence of a cDNA encoding the chicken p53 nuclear oncoprotein.

A:Reference number: S02193; MUID:89083584

A:Accession: S02193

A:Molecule type: mRNA

A:Residues: 1-367 <SOU>

A:Cross-references: EMBL:X13057; NID:963740; PIDN:CAA31456.1; PID:963741

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; nucleus; pho

F;366/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match 32.1% Score 764.5; DB 1; Length 367;

Best Local Similarity 44.6% Pred. No. 1.4e-51;

Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

Qy 11 LSP-EVQHTWDFLEQPICSVQPIIDNFVDEPSEDGATKRIEISMDCI RMQDSDLSPMP 69

Db 9 LEPTVEFMDSMLPY---SMOOL-----PLEPDSHWQELS-----PLEPDSPPPP 54

Qy 70 PLYNGLILNSMQOIQNGSSSTSPYNTDHAQNSVTAAPSPYAPSPSTF DALSPSPALP 129

Db 55 PPLPL-----AAAAPPLLP--TPPRAAPSPVPS 85

Qy 130 TDYPPGPISEPVSFQOSTAKSATWTYSTELKLYCOIAKTCPIQAKMTPPOGAVIRAM 189

Db 86 EDYGGDFEVGVFVGAETAKSYTCYISPLNKLFCOLAKTCPLAVRVE 145

Qy 190 PYKKAHEVTEYKRCPNHLSREFNEGOIAPPSHLIRKNSHAQYVEDPTGROSLV 249

Db 146 AVYKKEHVAEYKRCPIHRSERVEPGE-LAPAQHLIRKNSHAQYVEDPTGROSLV 204

Qy 250 PYPPQVGTFTVLYNFCNSCGVGNRRPILITVLETRDQVUGLRKCFEYAVACAP 309

Db 205 PYPPQVGTFTVLYNFCNSCGVGNRRPILITVLETRDQVUGLRKCFEYAVACAP 264

Qy 310 GRPKADEDSIRKQVSDSTKNGD--TKRPRQNTMHIQMTSIRKRSPPDELLYLPVR 367

Db 265 GRPKADEDSIRKQVSDSTKNGD--TKRPRQNTMHIQMTSIRKRSPPDELLYLPVR 367

Qy 368 GRETYEMLKKESTELMO 386

Db 317 GRRREYEMLKKESTELMO 335

RESULT 4

S51648

cellular tumor antigen p53 - bovine

N:Alternate names: tumor-suppressor protein p53

C:Species: Bos primigenius taurus (cattle)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S51648

R:dequiedt, F.; Williams, L.; Burny, A.; Kethmann, R.

submitted to the EMBL Data Library, September 1994

A:Description: Nucleotide sequence of the ovine p53 tumor-suppressor gene cDNA and its

A:Reference number: S51648

A:Accession: S51648

A:Molecule type: preliminary

A:Residues: 1-386 <DBO>

A:Cross-references: EMBL:X81704; NID:9602332; PIDN:CAA57348.1; PID:9602333

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotetramer; phosphoprote

F;168,171,231,235/Binding site: zinc (Cys, His, Cys, Cys) #status predicted

F;385/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	31.1%;	Score 741.5;	DB 1;	Length 386;
Best Local Similarity	38.4%;	Pred. NO. 9.1e-50;		
Matches 165;	Conservative 68;	Mismatches 126;	Indels 71;	Gaps 11;

RESULT 5

502192

cellular tumor antigen p53 - rat

N:Alternate names: gene p53 protein; nuclear oncoprotein p53

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: 502192; S41149

R:Soussi, T.; de Fromental, C.C.; Breugnot, C.; May, E.

A:Title: Nucleotide sequence of a cDNA encoding the rat p53 nuclear oncoprotein.

A:Reference number: 502192; MUID:89083585

A:Accession: 502192

A:Residues: 1-391 <SDU>

A:Molecule type: mRNA

A:Cross-references: EMBL:X13058; NID:g56828; PIDN:CAA31457.1; PID:g56829

R:Hulla, J.E.; Schneider, R.P.

Nucleic Acids Res. 21, 713-717, 1993

A:Title: Structure of the rat p53 tumor suppressor gene.

A:Reference number: S41149; MUID:93181268

A:Accession: S41149

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-173, 'W', 175-391 <HUL>

A:Cross-references: EMBL:L07909

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992

C:Genetics:

A:Introns: 25/2; 32/3; 123/3; 185/1; 259/2; 305/1; 329/3; 365/2

C:Superfamily: cellular tumor antigen p53

C:Keywords: apoptosis; cell division control; DNA binding; homotrimer; nucleus; phosph

C:1174,1177,236,240/Binding site: zinc (Cys, His, Cys, Cys) #status Predicted

C:1390/Binding site: phosphoryl-RNA (Ser) (covalent) #status predicted

Query Match	30.7%;	Score 732;	DB 1;	Length 391;
Best Local Similarity	42.0%;	Pred. No. 5e-49;		
Matches 162;	Conservative 64;	Mismatches 116;	Indels 44;	Gaps 11;

[illegible]

QY 191 VYKRAHTEVYKRCPNHETLREPNQIAPSPHLLRVGNSIAQYVEDPITGROSLVP 250
 Db 165 IYKKLQYWEVVRRCRPHERSSE-GDS-LAPPOHLLRVGNSHAEYLDKQCFRRHSVVP 222
 QY 251 YEPQVCTEFTYVLYNFMCSGCVGNNRRPILITVLETRDQOVYGRRCFARICACPG 310
 Db 223 YEPEVGSDDTTHYNNCMNSCGMGNRRPILITLEDPSGNLGRNSFEVRICACPG 282
 QY 311 RDRKADSDSIRKQVSDSTKNGDTRKPRPROMTHGIMSTIKRSRSPDELLYLPVGRG 370
 Db 283 RDRTEKRNQKGPCEPCLPRKSAKRALPTMT---SSSPQPKRRTLDGEFTTLKIRGOE 339
 QY 371 TYEMLLKIKESLEMLQYLQPHITE-----TYRQOQOQOHOHLQKHLISACFRNELVEP 424
 Db 340 RFKMFELNALLKDAQALKASDSCGASHSYLKSQKQSGASRLKMLI----- 388
 QY 425 RRETP 429
 Db 389 KREGP 393
 RESULT 7
 DNHUS3
 cellular tumor antigen p53 [validated] - human
 N:Alternate names: cellular phosphoprotein p53; oncoprotein p53; transformation suppressor
 C:Species: Homo sapiens (man)
 C:Date: 05-Oct-1988 #sequence revision 18-Nov-1994 #text change 15-Sep-2000
 A:Accession: A25224; A43073; J04036; S40773; S42669; A2837; A25060; A25397; B25397; S42
 4905; I58354; I52681; S60153
 R:Lamb, P.; Crawford, L.
 Mol. Cell. Biol. 6, 1379-1385, 1986
 A:Title: Characterization of the human p53 gene.
 A:Reference number: A25224; MUID:87064416
 A:Accession: A25224
 A:Molecule type: DNA
 A:Residues: 1-393 <LMB>
 A:Cross-references: EMBL:X01405; GB:M13121; GB:N00032; NID:9189460; PIDN:AA559987.1; PIT
 R:Buchanan, V.L.; Chumakov, P.M.; Ninkina, N.N.; Samarina, O.P.; Georgiev, G.P.
 Gene 70, 245-252, 1988
 A:Title: A variation in the structure of the protein-coding region of the human p53 gene
 A:Reference number: J04036; MUID:89108008
 A:Accession: A43073
 A:Molecule type: DNA
 A:Residues: 1-393 <BUC1>
 A:Cross-references: EMBL:M22898; NID:9189474
 A:Note: this 72-Arg allele appears to be about 5 times more frequent than the 72-Pro allele
 A:Accession: J04036
 A:Molecule type: DNA
 A:Residues: 1-71, 'P', '73-393 <BUC2>
 A:Cross-references: EMBL:M22898; NID:9189474; PIDN:AA559987.1; PID:9189476
 R:Chumakov, P.M.; Almazov, V.P.; Jenkins, J.R.
 submitted to the EMBL Data Library, August 1990
 A:Reference number: S40773
 A:Accession: S40773
 A:Molecule type: DNA
 A:Residues: 1-393 <CHU>
 A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
 R:MacLuski, G.; Lamb, P.; Pim, D.; Peacock, J.; Crawford, L.; Benchimol, S.
 EMBO J. 3, 3257-3262, 1984
 A:Title: Isolation and characterization of a human p53 cDNA clone: expression of the hum
 A:Reference number: S42669; MUID:85126934
 A:Accession: S42669
 A:Molecule type: mRNA
 A:Residues: 101-393 <MK11>
 A:Cross-references: EMBL:X01405; NID:935215; PIDN:CAA25652.1; PID:9642241
 R:Zakut-Hourli, R.; Bienert-Tadmor, B.; Givol, D.; Oren, M.
 EMBO J. 4, 1251-1255, 1985
 A:Title: Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells.
 A:Reference number: A2837; MUID:85230577
 A:Accession: A2837
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', '73-393 <ZAK>

A:Cross-references: EMBL:X02469; EMBL:M60950; NID:935209; PIDN:CAA26306.1; PID:935210
 R:Hartill, E.; Williamson, N.M.; Ralston, R.; Helfman, D.M.; Adams, T.E.
 Mol. Cell. Biol. 5, 1601-1610, 1985
 A:Title: Molecular cloning and in vitro expression of a cDNA clone for human cellular
 A:Reference number: A55060; MUID:85267676
 A:Accession: A55060
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', '73-272, 'H', '274-393 <HAR>
 A:Cross-references: GB:K03199; NID:9189478; PIDN:AA559989.1; PID:9189479
 R:Harris, N.; Brill, E.; Shohat, O.; Prokocimer, M.; Wolf, D.; Aral, N.; Rotter, V.
 Mol. Cell. Biol. 6, 4650-4656, 1986
 A:Title: Molecular basis for heterogeneity of the human p53 protein.
 A:Reference number: A3086; MUID:87089826
 A:Accession: A25397
 A:Molecule type: mRNA
 A:Residues: 1-78, 'T', '80-393 <HAR1>
 A:Cross-references: EMBL:M4694; NID:9339813; PIDN:AA61211.1; PID:9339814
 A:Experimental source: clone p53-H-1, transformed hydridoma SV-80 cell line
 A:Accession: B25397
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', '73-78, 'T', '80-393 <HAR2>
 A:Cross-references: EMBL:M4695; NID:9339815; PIDN:AA61212.1; PID:9339816
 R:Malashewski, G.J.; Tuck, S.; Pim, D.; Lamb, P.; Schneider, J.; Crawford, L.V.
 Mol. Cell. Biol. 7, 961-963, 1987
 A:Title: Primary structure polymorphism at amino acid residue 72 of human p53.
 A:Reference number: S42452; MUID:87144273
 A:Accession: S42452
 A:Molecule type: mRNA
 A:Residues: 66-71, 'P', '73-79 <MK12>
 A:Experimental source: clone lambda C113
 A:Note: 72-Cys was also found, and appears to represent a polymorphism
 A:Accession: S42453
 A:Molecule type: DNA
 A:Residues: 66-79 <MK13>
 A:Experimental source: clone J6K
 R:Farrell, P.J.; Allan, G.J.; Shanahan, F.; Vousden, K.H.; Crook, T.
 EMBO J. 10, 2870-2887, 1991
 A:Title: p53 is frequently mutated in Burkitt's lymphoma cell lines.
 A:Reference number: I38082; MUID:92007731
 A:Accession: I38082
 A:Molecule type: mRNA
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-189, 'L', '194-393 <F02>
 A:Cross-references: EMBL:X60010; NID:9506432; PIDN:CAA42625.1; PID:9506433
 A:Note: deletion of a C nucleotide causes a frameshift at position 566
 A:Accession: I38083
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-192, 'R', '194-393 <F02>
 A:Cross-references: EMBL:X60011; NID:9506434; PIDN:CAA42626.1; PID:9506435
 A:Accession: I38084
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-393 <F03>
 A:Cross-references: EMBL:X60012; NID:9506436; PIDN:CAA42627.1; PID:9506437
 A:Accession: I38085
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-245, 'T', '247-393 <F04>
 A:Cross-references: EMBL:X60013; NID:9506438; PIDN:CAA42628.1; PID:9506439
 A:Accession: I38086
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-236, 'T', '238-393 <F05>
 A:Cross-references: EMBL:X60014; NID:9506440; PIDN:CAA42629.1; PID:9506441
 A:Accession: I38087
 A:Status: translated from GB/EMBL/DBJ
 A:Residues: 1-247, 'Q', '249-393 <F06>
 A:Cross-references: EMBL:X60015; NID:9506442; PIDN:CAA42630.1; PID:9506443
 A:Accession: I38088

A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-237, 'Y', 239-393 <F07>
 A:Cross-references: EMBL:X60016; NID:9506444; PIDN:CAA42631.1; PID:9506445
 A:Accession: I38089
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-247, 'O', 249-393 <F08>
 A:Cross-references: EMBL:X60017; NID:9506446; PIDN:CAA42632.1; PID:9506447
 A:Accession: I38090
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-71, 'P', 73-162, 'H', 164-393 <F09>
 A:Cross-references: EMBL:X60018; NID:9506448; PIDN:CAA42633.1; PID:9506449
 A:Accession: I38091
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212, 'O', 214-393 <F10>
 A:Cross-references: EMBL:X60019; NID:9506450; PIDN:CAA42634.1; PID:9506451
 A:Accession: I38092
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-253, 'D', 255-393 <F11>
 A:Cross-references: EMBL:X60020; NID:9506452; PIDN:CAA42635.1; PID:9506453
 A:Note: all sequences submitted to the EMBL/GenBank/DBJ databases June 1991
 R:Futurel, P.A.; Barrett, J.C.; Wiseman, R.W.
 Nucleic Acids Res. 19, 6977, 1991
 A:Title: An Alu polymorphism intragenic to the TP53 gene.
 A:Reference number: I38093; MUID:92107726
 A:Accession: I38093
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-393 <FUT>
 A:Cross-references: EMBL:X54156; NID:935213; PIDN:CAA38095.1; PID:935214
 R:Yamada, Y.; Yoshida, T.; Hayashi, K.; Sekiya, T.; Yokota, J.; Hirahashi, S.; Nakatani, Cancer Res. 51, 5800-5805, 1991
 A:Title: p53 gene mutations in gastric cancer metastases and in gastric cancer cell line
 A:Reference number: A44905; MUID:92034678
 A:Accession: A44905
 A:Molecule type: DNA
 A:Residues: 246-247, 'W', 249-250 <YAM>
 A:Cross-references: GB:S63157; NID:9237829; PIDN:AAB20140.1; PID:9237830
 A:Note: sequence extracted from NCBI backbone (NCBI:63157, NCBI:63158)
 R:Hensel, C.H.; Xiang, R.H.; Sakaguchi, A.Y.; Naylor, S.L.
 Oncogene 6, 1067-1071, 1991
 A:Title: Use of the single strand conformation polymorphism technique and PCR to detect
 A:Reference number: I58354; MUID:91296386
 A:Accession: I58354
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 244-247, 'W', 249-252 <HEN1>
 A:Cross-references: GB:S41969; NID:91679931; PIDN:AAB19324.1; PID:9232814
 A:Accession: I78850
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 274-277, 'S', 279-282 <HEN2>
 A:Cross-references: GB:S41977; NID:91679932; PIDN:AAB19325.1; PID:9232816
 R:Chow, V.T.; Quek, H.H.; Jock, E.P.C.
 Cancer Lett. 73, 141-148, 1993
 A:Title: Alternative splicing of the p53 tumor suppressor gene in the Molt-4 T-lymphobla
 A:Reference number: I52681; MUID:94036762
 A:Accession: I52681
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 327-331, 'DQTSFQKENC', <CHO>
 A:Cross-references: GB:S66666; NID:9436292; PIDN:AAB28601.1; PID:9436293
 A:Note: mutant sequence with altered splicing and termination expressed in Molt-4 T-Lymp
 R:Peersen, G.; Song, D.; Hiegle-Doerr, B.; Oldenburg, I.; Bautz, E.K.F.
 Mol. Gen. Genet. 249, 425-431, 1995
 A:Title: Mapping of linear epitopes recognized by monoclonal antibodies with gene-fragme
 A:Reference number: S60151; MUID:96133682
 A:Accession: S60153

A:Molecule type: DNA
 A:Residues: 3-44 <PEP>
 R:Yang, C.V.; Lee, W.M.F.
 J. Biol. Chem. 264, 18019-18023, 1989
 A:Title: Nuclear and nucleolar targeting sequences of c-erb-A, c-myc, N-myc, p53, HSP
 Query Match 30.1%; Score 717.5; DB 1; Length 393;
 Best Local Similarity 41.2%; Pred. No. 6.7e-48;
 Matches 156; Conservative 60; Mismatches 116; Indels 47; Gaps 9;
 11 LSPEVFOHIMDFLEQPICSVQPIDLNFVDEPSEDEGATKRIEISMDICIMODSDLSDPMPW 70
 Db LSGERFSDLMKLP-----NNVLSPLPSQAMDMLSPDIDQWTE--D--- 58
 14 LSGERFSDLMKLP-----NNVLSPLPSQAMDMLSPDIDQWTE--D--- 58
 71 QYTNGLINSDQIQONSSSTSPYNTHAQNSVTAPEPYAPSPSTFALP-----SPA 126
 Db -----GPEAPMPPEAAR--VAAP--AAPPAAPAPASWPLSSV 97
 127 PSNTDYPGPHSPFVQSSSTAKSATWTSTELKLYCOIKTCPIQIKVTPPGAGAVI 186
 Db PSQKTYQSGYGFRLGFLHSGTAKSVCTTSPALNMFQOLAKTCVQVLWDSTPPGTRV 157
 187 RAMPYKRAEHVTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYEDPTTGROS 246
 Db RMAIYKQSQHWTEVVRRCPHHE--RCSDSQDLAPQQLIRVEGNLRVYLLDDRMTFRHS 215
 247 VLVPYEPQVGFETFTVLYNMCNCSYGVGNRRPILITVLETGQVLRGCFEATIC 306
 Db VVVPYEPPEVSDCTTTHYNYNCNCSGCMNRRPILITVLEDSGNLRNSENSEVAC 275
 307 ACPGRKRADEDSIRKQOVSDTKNGDGTKRPFQNTQIGMTSIRKRRSP--DDELLVLP 365
 Db ACPGRKRTTEENLNKKKEPHELPPGSTKRALPNT-----SSFPQKKKPLDGEYFTLG 331
 366 VGRGTEYMLKIKESLEL 384
 Db IRGRERFEMFRELNELEL 350
 RESULT 8
 DNMS53
 cellular tumor antigen p53 - mouse
 N:Alternate names: oncoprotein p53
 C:Species: Mus musculus (house mouse)
 C>Date: 28-Aug-1985 #sequence_revision 04-Oct-1996 #text_change 11-May-2000
 C:Accession: A22739; S06336; A02684; S38823; S40014; I48703
 R:Blenz, B.; Zakut-Houri, R.; Gliwol, D.; Oren, M.
 EMBO J. 3, 2179-2183, 1984
 A:Title: Analysis of the gene coding for the murine cellular tumour antigen p53.
 A:Reference number: A22739; MUID:85027173
 A:Accession: A22739
 A:Molecule type: DNA
 A:Residues: 1-134, 'V', 136-390 <BIE>
 A:Residues: 1-134, 'V', 136-390 <BIE>
 A:Cross-references: GB:X00876; NID:9871420; PIDN:CAA25420.1; PID:9871421; GB:X01237;
 R:Chumakov, P.M.
 Bioorg. Khim. 13, 1691-1694, 1987
 A:Title: Primary structure of DNA complementary to murine oncoprotein p53 mRNA.
 A:Reference number: S06336; MUID:88221682
 A:Accession: S06336
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-134, 'V', 136-390 <CHU>
 R:Zakut-Houri, R.; Oren, M.; Blenz, B.; Lavie, V.; Hazum, S.; Gliwol, D.
 Nature 306, 594-597, 1983
 A:Title: A single gene and a pseudogene for the cellular tumour antigen p53.
 A:Reference number: A02684; MUID:84068204
 A:Accession: A02684
 A:Molecule type: mRNA
 A:Residues: 1-159, 'H', 161-167, 'G', 169-233, 'T', 235-390 <ZAK>
 A:Cross-references: GB:X01237; GB:X01700; NID:953575
 R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.

A:Reference number: JC6176; MUID:97183659
 A:Contents: liver
 A:Accession: JC6176
 A:Molecule type: mRNA
 A:Residues: 1-393 <LEF>
 A:Cross-references: GB:50395; NID:g1842229; PIDN:AAC53040.1; PID:g1842230
 C:Comment: This protein is a multimer, it plays the central role in a complex DNA damage
 lition, and recombination by protein/protein interactions.
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: liver; tumor

Query Match 29.5%; Score 704; DB 2; Length 393;
 Best Local Similarity 38.6%; Pred. No. 7.4e-47;
 Matches 165; Conservative 66; Mismatches 134; Indels 60; Gaps 11;

QY 11 LSPEVQHINDLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCIKMODSDLSDPV-- 68
 DB 14 LSQETFDLWKTL-----PPNNVLSTLPSSDS-----IEELFISENVTG 52

QY 69 WPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAQPSSTFDALSPSPAIP 127
 DB 53 WLEDSGGAL-----QGVAAAAAST-----AEDPVETEPAPVASAPATPPLSS--VP 98

QY 128 SMDYGPSPVDFVQSSSTAKSATWTSTELTKLYCOIATCPIDIKVMPPPQGANVR 187
 DB 99 SYKTFQGDYGFRLGFLSLGSTRKSVCTYSPSLNFCOLATCPVOLWVNSTPPGTRVR 158

QY 188 AMPYKAEHYTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVDPTGRQSV 247
 DB 159 AMAFYKILQYVTEVVRRCPHHERSEGD--SLAPQHILIRVGNLHAEYLDKQTFHRSV 216

QY 248 LVPEPPQVGEFTVLYXNFNCSSCYGGMRRPILITVLETGQVGLGRCEARICA 307
 DB 217 VVPEPEVSGDCTTHYNWNCSSCGMNRPIILITLEDSSGNLGNSEFEVRICA 276

QY 308 CPGRDRADEDSIRKQVSDSTKNGDGTKRPRFRONTGICQMTSIKRRSPDELLYLPVR 367
 DB 277 CPGRDRTEENFQKGCPECELPKSAKRALPTNT---SSPPPKKTTLDGEYFTLKIR 333

QY 368 GRETEMLKIKESLELMQYLPQHTIE-----TYRQOQOQHQLKILKLSACFRNEL 421
 DB 334 GHERFKMFOELNEALELKDQAQSGSEDNCAHSSYLKSKGQASRLKILMI----- 385

QY 422 VEPREPT 429
 DB 386 ---KREGP 390

RESULT 11
 S38824
 cellular tumor antigen p53, minor splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S38824; S35478
 R:Arai, N.; Nomura, D.; Yokota, K.; Wolf, D.; Brill, E.; Shohat, O.; Rotter, V.
 Mol. Cell. Biol. 6, 3232-3239, 1986
 A:Title: Immunologically distinct p53 molecules generated by alternative splicing.
 A:Reference number: S38822; MUID:87064640
 A:Accession: S38824
 A:Molecule type: mRNA
 A:Residues: 1-381 <ARA>
 A:Cross-references: GB:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 R:Han, K.A.; Kulesz-Martin, M.F.
 Nucleic Acids Res. 20, 1979-1981, 1992
 A:Title: Alternatively spliced p53 RNA in transformed and normal cells of different tiss
 A:Reference number: S35478; MUID:92253421
 A:Accession: S35478
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-381 <HAN>

A:Cross-references: EMBL:M13874; NID:g200202; PIDN:AAA39883.1; PID:g200203
 A:Note: the nucleotide sequence was submitted to the EMBL data library, July 1988
 C:Comment: This sequence, produced by alternative splicing of the tenth intron, lacks
 s not known.
 C:Superfamily: cellular tumor antigen p53
 C:Keywords: alternative splicing; phosphoprotein; zinc
 F:1-44/Domain: transcription activation #status predicted <RA>
 F:16-26/Region: conserved region I
 F:99-289/Domain: DNA-binding core #status predicted <BC>
 F:108-121/Region: L1 loop
 F:114-139/Region: conserved region II
 F:160-192/Region: L2 loop
 F:168-178/Region: conserved region III
 F:231-252/Region: conserved region IV
 F:233-248/Region: L3 loop
 F:267-283/Region: conserved region V
 F:313-319/Region: nuclear location signal
 F:319-357/Region: tetramer association
 F:7,9,12,18,23,37/Binding site: phosphate (Ser) (covalent) #status predicted
 F:173,176,235,239/Binding site: zinc (Cys, His, Cys, Cys) #status predicted
 F:312/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted

Query Match 29.5%; Score 702; DB 2; Length 381;
 Best Local Similarity 40.4%; Pred. No. 1e-46;
 Matches 159; Conservative 58; Mismatches 113; Indels 64; Gaps 11;

QY 2 SOSYQVNEF-LSPEVQHINDLEOPICSVOPIDLNFEVDEPSEDGATNKIEISMDCIKMO 60
 DB 7 QSQDISLELPLSQETFFSLMKTL-----PPED-----LTPSPHC----- 40

QY 61 DSDSDPMPWPOYTNGLNSMDQOIONGSSSTPYNTDHAQNSVT-APSPYAQPSSTFD 119
 DB 41 ---MDLLLPQ-----DVEEFEGPSEALRVSGAPADPTETPGPVA----- 81

QY 120 LSPSPA-----IPSNVDYGPSPVDFVQSSSTAKSATWTSTELTKLYCOIATCP 171
 DB 82 --PAPATPWLSPSPVPSQKTYQGVNGFHLGFLQSGFAKSVCTYSPSLNFCOLATCP 139

QY 172 IQIVMPPPQGANVIRAMPYKAEHYTEVVKRCPNHELSEFNEGO-IAPPSHLIRVGN 230
 DB 140 VOLWVSATPSPVAGSRVAVALTKKSQHMTEVVRCPNHE--RCSDGDLAPQHILIRVGN 196

QY 231 NSHAQYVEDPTGRQSVLVPEPPQVGEFTVLYXNFNCSSCYGGMRRPILITVLET 290
 DB 197 NLYPEYLEDRTGTPRHSVYVPEPEPAGSEYTHYKYNCSGCMNRPIILITLED 256

QY 291 RDGVLGRCEARICACPGDRKRADEDSIRKQVSDSTKNGDGTKRPRFRONTGICQMTS 350
 DB 257 SSGNILGRDSEFVAVCACPGDRDRTEENFRKKEVLCPELPFGSAKRALPTCT---SASP 313

QY 351 IKRRSPDELLYLPVGRETEMLKIKESLEL 384
 DB 314 POKKRPDLGEYFTLKIRKRFEMFRELENALEL 347

RESULT 12
 JC6193
 tumor suppressor p53 - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000
 C:Accession: JC6193
 R:Le Gass, F.; May, P.; Ronco, P.; de Fromental, C.C.
 Gene 185, 169-173, 1997
 A:Title: cDNA cloning and immunological characterization of rabbit p53.
 A:Reference number: JC6193; MUID:97208869
 A:Accession: JC6193
 A:Molecule type: mRNA
 A:Residues: 1-391 <LEA>
 A:Cross-references: EMBL:X90592; NID:g1532043; PIDN:CAA62216.1; PID:g1532044
 C:Genetics:
 A:Gene: p53
 C:Superfamily: cellular tumor antigen p53

C:Keywords: tumor

Query Match 29.4%; Score 699.5; DB 2; Length 391;
 Best Local Similarity 39.3%; Pred. No. 1.6e-46;
 Matches 156; Conservative 56; Mismatches 102; Indels 81; Gaps 10;

QY 11 LSPVFOHIDFL-EOPICSVQ---PID-----LNVDPSEDEGATNKIEISMDICR 58
 DB 14 LSOFTSDYDKMLLPENNLITSLNPVVDLLSEADYANLNLNDEPBG----- 60
 QY 59 MODSDSDPMPOYTNGLNLSMDQOIQNGSSSTSPYNTDHAQNSVTAPSPAPQSSTFD 118
 DB 61 -----LRVP-----APPAEA-PAPAP 77
 QY 119 AL-SPSPA-----IPNTDYPGPHSPFVSFOQSTAKSTWTYSTEKLKYOQIAKT 169
 DB 78 ALAAPAPATSWPLSSVSPQKTYHGNFYGRGLGSLHSGTAKSVTCTYSPCLNKLFCQOLAKT 137
 QY 170 CPLOIKVMTPPGAVIRAMPYKKAHVTEVYKCPNHELREBNQOIAFPSHLIRVE 229
 DB 138 CPVQLWVDSTPPGTRVRAMALYKKSQHTTEVYRCPHHE--RCSDDGLAPPOHLIRVE 195
 QY 230 GNSHAQVEDPTTGROSLVLYPEPQVGTETTYLYNPMSCSSCGAMRRPLITITLLE 289
 DB 196 GMLRAEYLDNRFTFRSHSVVYEPPEVSGDCTTHYNTMCSGCMGMRPPLITITLLE 255
 QY 290 TFDGVLGRCEFEARICACRGDRKADSDIRKQVSDSTKNGDGTTRPROMTGIQMT 349
 DB 256 DSSGGLGRNFEVAVACACRGDRKADSDIRKQVSDSTKNGDGTTRPROMTGIQMT 349
 QY 350 SIKKRRSDDELVLVPAVGRETYEMLIKESLEL 384
 DB 314 POTKKKKPLDGEYFLTKIRGRERFEMRELNALEL 348

RESULT 13
 146226
 cellular tumor antigen p53 - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-May-2000
 R:Accession: 146226
 R:Deviljee, P.; Van Leeuwen, I.S.; Voesten, A.; Rutteman, G.R.; Vos, J.H.; Cornelisse, C.
 Anticancer Res. 14, 2039-2046, 1994
 A>Title: The canine p53 gene is subject to somatic mutations in thyroid carcinoma.
 A:Reference number: 146226; MUID:95150524
 A:Accession: 146226
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-77 <DEV>
 A:Cross-References: GB:L27630; NID:q508454; PIDN:AAC37327.1; PID:q508455
 C:Genetics:
 A:Gene: p53
 A:Introns: 24/1; 61/3
 C:Superfamily: cellular tumor antigen p53

Query Match 10.9%; Score 259.5; DB 2; Length 77;
 Best Local Similarity 60.3%; Pred. No. 1.8e-13;
 Matches 47; Conservative 16; Mismatches 14; Indels 1; Gaps 1;
 QY 194 KAEHTEVYKCPNHELREBNQOIAFPSHLIRVEGNSHAQVEDPTTGROSLVLYPEP 253
 DB 1 KSEVTEVYRCPHHEKCSDDSDG-LAPPOHLIRVEGNSLAKYLDRTYFRHSVYVPEP 59
 QY 254 PÖVGTEFTYLYNPMCS 271
 DB 60 PEVGEFTYTHYNYMCS 77

RESULT 14
 T42730
 Bassoon protein - mouse

C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: T42730
 R:Dieck, S.; Sammarti-Vila, L.; Langanaese, K.; Richter, K.; Kindler, S.; Soyke, A.; W
 J. Cell Biol. 142, 499-509, 1998
 A>Title: Bassoon, a novel zinc finger CAG/Glutamine-repeat protein selectively local
 A:Reference number: 222249; MUID:98345363
 A:Accession: T42730
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-3942 <DIE>
 A:Cross-References: EMBL:Y17034; NID:93413809; PIDN:CAA76598.1; PID:93413810
 C:Genetics:
 A:Map position: 9p1
 A:Introns: 72/3; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
 A:Note: component of the presynaptic cytoskeleton
 C:Keywords: coiled coil; zinc finger

Query Match 4.8%; Score 114.5; DB 2; Length 3942;
 Best Local Similarity 21.2%; Pred. No. 7.3; Mismatches 190; Indels 169; Gaps 25;
 Matches 113; Conservative 61

QY 1 MSQSTQTFNEFISPEVPOHIDFLFOPT-----CSVOPIDLNVDPSEDP----- 44
 DB 2038 LGGLOYGSTFD---LRHPPDLISHPLPLRRYSVSNITSDHRYGPRDVGFOEASLQ 2094
 QY 45 -GATNKIEISMDICRIMQDSDLPMPPOYTNGLNLSMDQO-IQNGSSSTSP-----TNTD 98
 DB 2095 YSATAREISRM-----AALNSMDQYGGKHSGGSGGLVQYPOQ 2135
 QY 99 HAQNSVTAPSPYAPQSS-----TFDALSPPAISNTDYPGPHSPFVSFOQSTAKSAT 152
 DB 2136 HGP-GLSAGQGLAPLRSLGLGNPTPEGOPS---PGNLAQCPAASQATAVRQLPSTAT 2191
 QY 153 -----WYSTEKLKLYQIAKTCPIQIR---VMTPPGAVIRAMPYKKAHVTEVYK 203
 DB 2192 VRAADCMYST---INPIAATLPTTQPASVLRPMVRGMTR-----PYVSGGYT 2239
 QY 204 RCPNHELREBNQOIAFPSHLIRVEGNSHAQVEDPTTGROSLVLYPE-PPQY 257
 DB 2240 AVPLSLTR---VPMIARVPLGPAVLYRYPAPRT-----PIA---SSVPAEGPVYLG 2287
 QY 258 TEFTVLYNPMSCSSCGAMRRPILYIVLETRDGOVLGRCEFEARICACRG----- 310
 DB 2288 KPAAT-----KASGAGCPRPRLPAGVAREPFTTAPAVIKAPVAPAPAPAPPP 2340
 QY 311 -----RDKRADDSTIRKQVSDSTKNGDGTTRPROMTGIQ 347
 DB 2341 GOKPAGEAAGSGCVLSRPAKEKEASQEDRQKOE-----Q 2379
 QY 348 MTSIKKRRSDDELVLVPAVGRETYEMLIKESLEMOYLPOHTLET 395
 DB 2380 LQIERRVELEKIRQIRLOELERREVELQRHREBQGL--VQHELQLOITKOHVLD 2436
 QY 396 YRQOQOQOHLQKHLISACFNELVEPRREPQSDVFFHNSAPPNRYYP 448
 DB 2437 -QOQEEHQAQFALQREGLAQ--QRDLQEOIQOQOQLOQLEQOKOROKAPPP 2486

RESULT 15
 T32008
 hypothetical protein K106.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32008
 R:Davidson, S.; Wohlmann, P.; Mullen, G.
 submitted to the EMBL Data Library, July 1997
 A:Description: The sequence of C. elegans cosmid K106.

A:Reference number: 221111
A:Accession: T32008
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1819 <DNA>
A:Cross-references: EMBL:AF016669; PIDN:AAB66098.1; GSPDB:GN00020; CESP:K10G6.3
A:Experimental source: strain Bristol N2; clone K10G6
C:Genetics:
A:Gene: CESP:K10G6.3
A:Map position: 2
A:Introns: 41/2; 191/2; 556/2; 701/2; 1645/2; 1700/2; 1768/1; 1797/3

Query Match 4.7% Score 111.5; DB 2; Length 1819;
Best Local Similarity 19.4% Pred. No. 4.2;
Matches 76; Conservative 65; Mismatches 153; Indels 97; Gaps 15;

```
OY 84 QIONGSSSTPYNTDHAONS--VTAP-SPYAQPSITFDALSPSPAIPSNMDYPGPHSFDV 140
   ::|||:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 749 KVAASSSSNSASRPPQSPSTPATAPATPMLQASQAPQPLQAPPSMET-----TATV 802
OY 141 SFOOSSTAKSATWTYSTELKLLYCOIAKTCPIQIKMTPPQGAVTRAMPVYKKAENYTE 200
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 803 TYRTTYPPSVANTWTEKAQLISPKPRSQIFSEASSMTVGDLRAQCHQOKMDQIQ 862
OY 201 V-----VKRCPNHELSEFNEGQIAPPSHLI-----RVEGNSHAQYVEDPITGROS 246
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 863 IOFOQOQOQRFQNHQOQOQAGRIPPRRPPIILNOYONPQOVQNHQONOMLPI--RQP 920
OY 247 VL--VPEPPOVGETFTTVLYNFMCNSSCVGMNRRPILIIVT---LETROGVLGRRRC 300
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 921 LLAGPPPPPKKGLI-----EKKNTDLVLTSEPLAERMDAK---RRS 960
OY 301 FEARICA-----CPGRDKADEDSIRKQVSDSTKNGDGTKRPFRONTHG 345
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 961 SEGIAVATSTPLPPIQLPQRSQAPAPSRQOQOQPPVAYQVQNGRPLRPMLPPLQNPIN 1020
OY 346 IQMTSIKKRRSPDELLYLVPVGRGTEYMLIKESLELMOYLPOHTIETYROO--QQQ 403
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1021 QQ-----QOHOMLHQSQMNTIQOVQVQD--VQHVQOQOQNLQNO 1056
OY 404 HQHLLQKHLLSACFRNELVEPRRETPKQSDV 434
   ||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1057 HHHQQHQQ-----QNOQQAQGNRSRSHSNV 1082
```

Search completed: August 8, 2001, 01:37:49
Job time: 4655 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 01:35:41 : Search time 51.14 Seconds
(without alignments)
300.087 Million cell updates/sec

Title: US-09-670-568b-1

Sequence: 1 MSQSTQTNFLSPLEVFQHIW.....PKSDVFRHRSKPPNRSVYP 448

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1297.5	54.4	636	1 P73_HUMAN	O15350 homo sapien
2	1296.5	54.4	637	1 P73_HUMAN	O15350 homo sapien
3	847.5	35.6	396	1 P53_ONCMY	P25035 oncorhynch
4	819.5	34.4	369	1 P53_BARBU	O96678 barbus barb
5	805.5	33.8	373	1 P53_BRARE	P79734 brachydanio
6	800	33.6	376	1 P53_ICTPU	O83379 ictalurus p
7	777.5	32.6	363	1 P53_XENLA	P07193 xenopus lae
8	776	32.6	367	1 P53_TETMU	O96679 tetraodon m
9	770	32.3	386	1 P53_FELCA	P41685 felis silve
10	767	32.2	386	1 P53_PIG	O97424 sus scrofa
11	764.5	32.1	367	1 P53_CHICK	P10360 gallus gall
12	753.5	31.6	381	1 P53_CANFA	O29537 canis fami
13	746	31.3	351	1 P53_ORVLA	P79820 oryzias lat
14	741.5	31.1	386	1 P53_BOVIN	O29628 bos taurus
15	736	30.9	391	1 P53_MARMO	O36006 marmota mon
16	732	30.7	391	1 P53_RAT	P10361 rattus norv
17	730.5	30.7	391	1 P53_CAVPO	O29426 cavia porce
18	729.5	30.6	393	1 P53_TUPCB	O97424 tupia glis
19	727.5	30.5	382	1 P53_SHEEP	P11664 ovis aries
20	719.5	30.2	396	1 P53_MESAU	O00366 mesocricetu
21	718	30.1	366	1 P53_PLAFE	O12946 platichthys
22	717.5	30.1	393	1 P53_HUMAN	P04637 homo sapien
23	715.5	30.0	393	1 P53_MACRA	P66442 macaca fasc
24	715	30.0	390	1 P53_MOUSE	P02340 mus musculu
25	714.5	30.0	393	1 P53_CERAE	P13481 cercopithec
26	713.5	29.9	393	1 P53_MACMU	P56424 macaca mula
27	710.5	29.8	342	1 P53_XIPHE	O29538 xiphophorus
28	709.5	29.8	342	1 P53_XIPMA	O29143 xiphophorus
29	708	29.7	393	1 P53_CRICR	O09185 cricetus
30	699.5	29.4	391	1 P53_RABIT	O29330 oryctolagus
31	696	29.2	314	1 P53_SPEBB	O64662 spermophilu
32	689.5	28.9	280	1 P53_HORSE	P79892 equus caball
33	591.5	24.8	207	1 P53_EQUAS	O29480 equus asinu

ALIGNMENTS

RESULT 1	P73_HUMAN	STANDARD:	PRT: 636 AA.
AC	O15350:O15351; Q9NTR8.		
DT	01-OCT-2000 (Rel. 40, Created)		
DT	01-OCT-2000 (Rel. 40, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	TUMOR PROTEIN P73 (P53-LIKE TRANSCRIPTION FACTOR) (P53-RELATED PROTEIN)		
GN	TP73 OR P73.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eularchia; Primates; Carnivora; Hominoidea; Homo.		
OX	NCBI_TaxID=9606;		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).		
RC	TISSUE=Colon;		
RX	MEDLINE=97433090; PubMed=9288759;		
RA	Kaghad M., Bonnet H., Yang A., Creancier L., Biscan J.-C., Valent A.,		
RA	Minty A., Chalon P., Lelias J.-M., Dumont X., Ferrara P., McKeon F.,		
RA	Caput D.;		
RT	"Monoclonally expressed gene related to p53 at 1p36, a region		
RT	frequently deleted in neuroblastoma and other human cancers.";		
RL	Cell 90:809-819(1997).		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	MEDLINE=99289209; PubMed=10362363;		
RA	Yoshikawa H., Nagashima M., Khan M.A., McKenamin M.G., Hagihara K.,		
RA	Harris C.C.;		
RT	"Mutational analysis of p73 and p53 in human cancer cell lines.";		
RL	Oncogene 18:3415-3421(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).		
RX	MEDLINE=98389621; PubMed=9721206;		
RA	Mai M., Huang H., Reed C., Qian C., Smith J.S., Alderete B.,		
RA	Jenkins R., Smith D.I., Liu W.;		
RT	"Genomic organization and mutation analysis of p73 in		
RT	oligodendrogliomas with chromosome 1 p-arm deletions.";		
RL	Genomics 51:359-363(1998).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORMS GAMMA AND DELTA).		
RC	TISSUE=Neuroblastoma;		
RX	MEDLINE=99021697; PubMed=9802988;		
RA	De Laurenzi V., Costanzo A., Barcaroli D., Terrinoni A., Falco M.,		
RA	Anticichiarico-Petruzzelli M., Leviero M., Melino G.;		
RT	"Two new p73 splice variants, gamma and delta, with different		
RT	transcriptional activity.";		
RL	J. Exp. Med. 188:1763-1768(1998).		
RN	[5]		
RP	SEQUENCE FROM N.A. (ISOFORMS EPSILON AND ZETA).		
RC	TISSUE=Lymphocytes, Breast cancer, Hepatoma, and Skin;		
RX	MEDLINE=99310936; PubMed=10381648;		
RA	Costanzo A., Leviero M., Knight R.A.;		
RA	"Additional complexity in p73: induction by mitogens in lymphoid cells		
RT	and identification of two new splicing variants epsilon and zeta.";		

005192 drosophila
P40872 bacillus su
P23468 homo sapien
O00409 homo sapien
P49415 drosophila
P20134 saccharomyc
P22082 saccharomyc
O24167 drosophila
P29555 drosophila
P28478 turnip yell
P18850 homo sapien
P48423 drosophila

[illegible]


```
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: M75145; AAA49605.1;
DR PIR: JH0631; JH0631.
DR HSSP: P04637; JH0631.
DR InterPro: IPR002117;
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 90 281 BY SIMILARITY.
FT FT 325 356 OLIGOMERIZATION.
FT FT 325 356 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 396 AA; 43966 MW; 8422250765545A1C CRC64;

Query Match 35.6%; Score 847.5; DB 1; Length 396;
Best Local Similarity 45.4%; Pred. No. 1e-56;
Matches 181; Conservative 61; Mismatches 102; Indels 55; Gaps 10;

OY 11 LSPVFOHIDFLEOPICVQPIIDLNFDPEPSDGAFTKRIEIMDCIRMDSDLDSPMP 70
DB 12 LQSESPFDL-----KMINLVAVQPERE-----SWV 39
OY 71 QYTNLGLNLSMDQIOINGSSSTSPYNTDHAQNSVTPAPSAOPS-STPDALS-PSPAIPS 128
DB 40 GYDNF-----MMEAPLQ-----VFDPDSLEFVSKTEPAQPSSTLDTGSPSTVPT 87
OY 129 NTQYPGPHSDVFOOSSSTAKSATMTYSTELKKLYCOIAKTQPIQIKWTPPGAGAVIRA 188
DB 88 TSYRPAALGQLKELSSSTAKSVTCYSPDLNKLFCQIAKTQPIQIVDHPRPAGAVIRA 147
OY 189 MPYKKAHEVTEYVRCRPHNELSREFNEQIAPSHLRIVGNSHAQVVEPDTGRQSVL 248
DB 148 LAITYKLSADVAVRCRPHNOSTSENEGP-APRGHLVREVSNGRSEYMEDGNTLRHSVL 206
OY 249 VVEPPOVTEFTYLYNFMNCSGVGMNRRPILITVLETRDQVYGRRCFARICAC 308
DB 207 VVEPPOVSECTYLYNFMNCSGVGMNRRPILITVLETRDQVYGRRCFARICAC 266
OY 309 PGDRKADDSIRKQO---VSDSTKNSGCTKRPRQ--NTHGICMTSTIKRRS---PDDE 360
DB 267 PGDRKTEINIKKQOETTLTKTPAGGIRKRAKEASLPAPDQGASKTKSSPAVSDE 326
OY 361 LLYLVGRGETYEMLKIKESLELMQYLPQHTIETVYRQ 399
DB 327 IYTLQIRKEKEYEMLKFNDSLELSELYPVADADKYRQK 365

RESULT 4
P53_BARBU STANDARD; PRT; 369 AA.
AC 096678;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Barbus barbus (Barbel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Cyprininae; Barbus.
OX NCBI_TaxID=40830;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhaskaran A., May D., Rand-Weaver M., Tyler C.R.;
RT "Evolutionary conservancy of p53 gene sequences in fish.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL: AF071570; AAD34212.1;
DR InterPro: IPR002117;
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNAS_BIND 90 281 BY SIMILARITY.
FT FT 325 356 OLIGOMERIZATION.
FT FT 325 356 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 303 318 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 395 395 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 369 AA; 41233 MW; 0BE2CF2C2A74C304 CRC64;

Query Match 34.4%; Score 819.5; DB 1; Length 369;
Best Local Similarity 51.2%; Pred. No. 1.2e-54;
Matches 167; Conservative 49; Mismatches 87; Indels 23; Gaps 8;

OY 84 QIONGSSSTSPYNTDHAQNSV-APSPYAQPSSTFDALSPPAIPSTNDYPGPHSDVSE 142
DB 26 ELINDEYLPSSFDPIFDVLEQPOPTSP-----PTASVPVADYDVGEGFKLGF 77
OY 143 QOSSTAKSATMTYSTELKKLYCOIAKTQPIQIKWTPPGAGAVIRAMPVKKKAHEVY 202
DB 78 POSGTAKSVTCYSSDLNKLFCQIAKTQPIQIVMNVAPQGSVIRATAIYKSSHAHEVY 137
OY 203 KCRPHNELSREFNEQIAPSHLRIVGNSHAQVVEPDTGRQSVLYVPPPOVGTETFT 262
DB 138 RRCRPHERTPD-GGS-LAPAAHLIRVGNRSALYREDVNSRHSVVPYEVPLDGESEFT 195
OY 263 VLYNFMNCSGVGMNRRPILITVLETRDQVYGRRCFARICACGRRKADDESIRK 322
DB 196 VLYNFMNCSGVGMNRRPILITVLETRDQVYGRRCFARICACGRRKADDESIRK 255
OY 323 QOVSDFSTKNGD---GTRKRP-ROHTGICMTSTIKRR---SPDELLYLVGRGETY 373
DB 256 DQ---EKTIDKITSAAKRSITLDOSTSVPRPGSKRAKLSSGSDDEIYTLAVRGKERYE 312
OY 374 MLKIKESLELMQYLPQHTIETVYRQ 399
DB 313 MLKIKESLELMQYLPQHTIETVYRQ 338
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RESULT 5
P53_BRAE STANDARD; PRT; 373 AA.
ID P53_BRAE
AC P79734;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97344388; PubMed=9200835;
RA Cheng R., Ford B.L., O'Neal P.E., Mathews C.Z., Bradford C.S.,
RA Thongfuan T., Barnes D.W., Hendricks J.D., Bailey G.S.;
RT "zebrafish (Danio rerio) p53 tumor suppressor gene: cDNA sequence and
RT expression during embryogenesis.";
RL Mol. Mar. Biol. Biotechnol. 6:88-97(1997).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
DR EMBL; U60804; ABA40617.1; -
DR HSSP; P04637; ITR.
DR ZFIN; ZDB-GENE-990415-32; tp53.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 31 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 70 260 BY SIMILARITY.
FT DOMAIN 301 332 OLIGOMERIZATION.
FT DOMAIN 345 366 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 280 296 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 372 372 PHOSPHORYLATION (BY SIMILARITY).
SO SEQUENCE 373 AA; 41899 MW; AC7AB724FA6B1EF CRC64;
Query Match 33.8%; Score 805.5; DB 1; Length 373;
Best Local Similarity 53.9%; Pred. No. 1,4e-53;
Matches 158; Conservative 42; Mismatches 82; Indels 11; Gaps 4;
QY 112 QPSSTFALSPAIPTSDYRGPHSPFVSQSSSTASATWSTELKTKYQIAKCP 171
DB 55 QPST---LPTSTVPESTDPGDHGRFLRPQSGTASVCTTSPDLNKLFCQIAKCP 110
QY 172 IOIKVMPPOGAVIRAMPVYKKAHVTEVVKRCPNHELSEFNEGQIAPPSHLIRVEGN 231

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RESULT 6
P53_ICTPU STANDARD; PRT; 376 AA.
ID P53_ICTPU
AC 093379;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99071979; PubMed=9854815;
RA Luft J.C., Bengten E., Clem L.W., Miller N.W., Wilson M.R.;
RT "Identification and characterization of the tumor suppressor p53 in
RT channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 120B:675-682(1998).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC -----
DR EMBL; AF074967; AAC26824.1; -
DR HSSP; P04637; ITR.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1 36 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 77 268 BY SIMILARITY.
FT DOMAIN 303 334 OLIGOMERIZATION.
FT DOMAIN 347 372 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 286 298 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 375 375 PHOSPHORYLATION (BY SIMILARITY).
QY 349 --TSIKRRSPDELLYLPVRRGTEYEMLTIKESLEMOYLPQHTIETVYRQ 399
DB 289 EGSKKAKOSSSDEFLTQVARGREYELTKLNDLSQVDPASDAEKYRQK 341
QY 111 VQMYVDVAPPGSGVYRAIRATIKKSEHVAEYVRCPHH--RTPOGDNLAAPGHLIRVEGN 168
QY 232 SHAOYVEDPITGRQSVLVPPEPVGTEFTTLYVPMCNSSCGVMNRPILITVLETR 291
DB 169 QRANVREDNITLRLHSVFEPYAPOLGAEMTVLLNVMCNSSCGVMNRRPILITVLETO 228
QY 292 DGVLVGRCEFAKICACGRRKADDEDSIRK-QQVSDSTKGGDCTKRFRNTGION-- 348
DB 229 EGQLLGRSFEEVRCACGRCRDKTEESNFKDQETKMTAKTTTGTKSLVNESSATLRP 288
QY 349 --TSIKRRSPDELLYLPVRRGTEYEMLTIKESLEMOYLPQHTIETVYRQ 399
DB 289 EGSKKAKOSSSDEFLTQVARGREYELTKLNDLSQVDPASDAEKYRQK 341

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SEQUENCE 376 AA; 41989 MW; 1B89CD98DB3289F2 CRC64;

Query Match

Best Local Similarity 33.6%; Score 800; DB 1; Length 376;
Matches 164; Conservative 45; Mismatches 94; Indels 20; Gaps 5;

QY 108 SPYAPSPSTFDLSPSPAIIPSMNDYDGPSPVSPFOSSSTAKSATWYSTEKLKLYCOIA 167
DB 56 SDMLQPOSS--SSPSTVPIVSDYPLGLINLTFHOFESSGKTSVCTSPDLNLFQOLA 113
QY 168 KPCPIQIXMTPPGCAVIRAMPVYKKAHEVYKRCPNHLSRENEGOIAPSHLIR 227
DB 114 KICPVLMAVSSPPSGSVLRAVAYKREHVAEYVRRCPHHERNSDSDGP-APPGLHLR 172
QY 228 VEGNSHAQVYEDPIGRSVLVPYEPPOVGEFTVLYNFCNCCVCGANRRPILITVT 287
DB 173 VEGNSRAVYOEDGNTQANSVVPYPPVGSOSTVLYNWCNCCVCGANRRPILITIT 232
QY 288 LETRGQVYGRRCFARICACPGDRKADSDSIRKQOVSSTKNGDGTCKRPFQNTHTG 347
DB 233 LETQGHLLGRKTFEVRACACPGDRKTEESNFKKO-EPRTSGKTLTKRSMDDPSHPE 291
QY 348 MTSIKRRSPDELLYLPRGRETYEMLIKESLEMOYLPHQTTITYRQOQOQOHL 407
DB 292 ASKSKSNSSDDEITYTLQVRGKEREFELKINDGLSDVVPADDEKYROR----- 343
QY 408 LQKHLISACFRNE----LVEPRR 426
DB 344 ----LLSKTCRKRERDGAAGEPKR 362

RESULT 7
P53_XENLA STANDARD; PRT; 363 AA.

AC P07193;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8143684; PubMed=2830576;
RA Soussi T., de Fromental C.C., Mechali M., May P., Kress M.;
RT "Cloning and characterization of a cDNA from Xenopus laevis coding
RT for a protein homologous to human and murine p53.";
RT Oncogene 1:71-78(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94134403; PubMed=8302570;
RA Hoefer M., Clement J.H., Medlich D., Montenath M., Knoechel W.;
RT "Overexpression of wild-type p53 interferes with normal development
RT in Xenopus laevis embryos.";
RN Oncogene 9:109-120(1994).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND BAX ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.

CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.

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DR EMBL; M36962; AAA49923.1; -
DR EMBL; X05191; CAA28821.1; -
DR EMBL; X77546; CAA54672.1; -
DR EMBL; S68353; AAC60746.1; -
DR PIR; A29376; A29376.
DR HSSP; P04637; IISR.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
FT DOMAIN 1
FT DNAS_BIND 76
FT FT 267
FT DOMAIN 300
FT FT 331
FT DOMAIN 344
FT FT 356
FT FT 281
FT MOD_RES 362
FT FT 362
FT FT 52
FT FT 52
FT CONFLICT 71
FT FT 71
FT CONFLICT 296
FT FT 296
SQ SEQUENCE 363 AA; 40692 MW; CE1F3E58F020D74D CRC64;

Query Match 32.6%; Score 777.5; DB 1; Length 363;
Best Local Similarity 42.5%; Pred. No. 1.7e-51;
Matches 171; Conservative 55; Mismatches 95; Indels 81; Gaps 11;

QY 2 SOSGQNEFLSPVPOHIDFLEQPT---CSVPTDINFEVDEPSEDGATKRIEISMCI 57
DB 4 SSETGMDPPLSQDTEFDLWLSLPDLPQVTCRLDNLIS-EFPDYP-----LAADMT 52
QY 58 RMQDSDLSPMWFQYINLILNLSMDQIQNGSSSTSPYNTDHAQNSVTAAPVAPSSSTF 117
DB 53 VLQE-----GLMGN-----AVPTV- 67
QY 118 DALSPSPAIIPSMNDYDGPSPVSPFOSSSTAKSATWYSTEKLKLYCOIAKTCPIQIKVM 177
DB 68 -----SCAVPSTDDYAGKYGQLDFQNGTAKSVCTYSPELNLFQGLAKTCPLAVRE 122
QY 178 TEPPOGAVIRAMPVYKKAHEVYKRCPNHLSRENEGOIAPSHLIRVEGNSHAQVY 237
DB 123 SPPPGSILIRATAVYKKEHVAEYKRCPHHERSVGEF-DAAPSHLMEVEGNLAQVYA 181
QY 238 EDPINGRSVLYVPPVPGVGEFTVLYNFCNCCVCGANRRPILITVILETRDQOVIG 297
DB 182 EDVNSGRHSVCVPEPGVGEFTVLYNFCNCCVCGANRRPILITVILETRDQOVIG 241
QY 298 RRCFEARICACPGDRKADSDS-IRKQOVSSTKNGDGTCKRPFQNTHTG-GLQMSIKRR 354
DB 242 RRCFEVAVACACPGDRKTEEDENYTKKGLRPSGK-----RELHPSSSPLPKRR 292
QY 355 R---SPDELLYLVRGRETYEMLIKESLEMOYLPHQTTI 393
DB 293 LVVVDDEEITFLIRKGRSREYEMLIKINDALELOESLDQKV 334

RESULT 8
P53_TETMU STANDARD; PRT; 367 AA.
ID P53_TETMU
AC Q9W679;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)

DR PRINTS: PR00386; P53SUPPRESSOR.
 DR PROSITE: PS00348; P53: 1.
 KM Anti-oncogene: DNA-binding; Transcription regulation; Activator;
 KM Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 285 285 K -> R (IN REF. 2).
 SO SEQUENCE 386 AA; 42692 MW; D08B43BA1BC8EB78 CRC64;

Query Match 32.3%; Score 770; DB 1; Length 386;
 Best Local Similarity 42.1%; Pred. No. 6.7e-51;
 Matches 161; Conservative 58; Mismatches 103; Indels 60; Gaps 7;

QY 11 LSPVPHOHIMDELPICVOPIDLVFVDEPSEDGATNKIEISMDICRMQSDLSDEPMP 70
 DB 14 LSGETFSDELMKLPE-----NNVLSSELSSAMNELPSED-----48
 QY 71 QYTNGLNLSMDQOIONGSSSTSPYNTDHAQNSVAPSPYQPSSTFDALSPSPAT----126
 DB 49 -----VANMLDEA-----PDDASGMAVAPAPAPAPAT-----PAPATSWPL 85
 QY 127 -----PSNTDYGPSPFVSFOOSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTPPPO 182
 DB 86 SSFVPSQTYTGAGTGHGFLGSGTAKSVCTYSPPLNKLFQIAKTCPIQIAKTVMSRPPPP 145
 QY 183 GAVIRAMPVYKKAHVTEYVRCRNHLSREFNEGOIAPSHLIRVEGSHAOYVEDPT 242
 DB 146 GTCVRAVAITYKKSSEFMTEVVRCPHHERCPDSDG-LAPPOHLIRVEGSHAOYVEDPT 204
 QY 243 GROSIVLYPEPPVGYTEFTVLYNPMCNSSCGVGNRRPILITVLETRDGOVLGRCE 302
 DB 205 FRHSVYVPEPEVSGSCITHTNFMCNNSCGMNRPIITITLEDNGKILGRNPE 264
 QY 303 ARICACGRDKADEDSIRKQVSDSTKNGDTRKPRFRONTGIDQWTSIKRRSPDELL 362
 DB 265 VRCVACGRRDRTEENFRKRGCEPPPGSTRKALPST-----SSTPOKKKKPLDGEYF 321
 QY 363 YLVRGGEYEMTLKIKESLEL 384
 DB 322 TLQIRGRERFERLEALEL 343

RESULT 10
 P53_PIG
 ID P53_PIG STANDARD: PRT: 386 AA.
 AC 09TUB2;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53 OR P53.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burr P.D., Arzlye D.J., Reid S.W.J., Nasir L.;
 RT "Nucleotide sequence of the pig p53 tumor suppressor cDNA";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF

CC BAX AND BCL-2 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION.
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: AF098067; AAF04620.1;
 CC DR InterPro: IPR002117;
 CC DR Pfam: PF00870; P53: 1.
 CC DR PRINTS: PR00386; P53SUPPRESSOR.
 CC DR PROSITE: PS00348; P53: 1.
 CC KM Anti-oncogene: DNA-binding; Transcription regulation; Activator;
 CC Nuclear protein; Phosphorylation; Apoptosis.
 CC FT DOMAIN 1 45 TRANSCRIPTION ACTIVATION (ACIDIC).
 CC FT DNA_BIND 94 285 BY SIMILARITY.
 CC FT DOMAIN 318 349 OLIGOMERIZATION.
 CC FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 CC FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 CC SO SEQUENCE 386 AA; 42692 MW; AAC3DB8BDF55162 CRC64;

Query Match 32.2%; Score 767; DB 1; Length 386;
 Best Local Similarity 38.6%; Pred. No. 1.1e-50;
 Matches 167; Conservative 69; Mismatches 125; Indels 72; Gaps 10;

QY 11 LSPVPHOHIMDELPICVOPIDLVFVDEPSEDGATNKIEISMDICRMQSDLSDEPMP 70
 DB 14 LSGETFSDELMKLPE-----NNVLSSELSSAMNELPSED-----48
 QY 71 QYTNGLNLSMDQOIONGSSSTSPYNTDHAQNSVAPSPYQPSSTFDALSPSPAT----126
 DB 49 -----VTNMLDENPDDASRVAP-----PAPAPAPAPAPATSWPL--SSFVPSOK 93
 QY 131 DYGPSPFVSFOOSTAKSATWYSTEKLKLYCOIAKTCPIQIKVMTPPQGVIRAMP 190
 DB 94 TYPGSTDFRLGFLHSGTAKSVCTYSPALNKLFCQIAKTCPIQIAKTVMSRPPPPGRVAMA 153
 QY 191 YKKAHVTEYVRCRNHLSREFNEGOIAPSHLIRVEGSHAOYVEDPTGRQSYLV 250
 DB 154 LYKKESEYMEVYVRCRNHLSREFNEGOIAPSHLIRVEGSHAOYVEDPTGRQSYLV 212
 QY 251 YEPVGVTEFTVLYNPMCNSSCGVGNRRPILITVLETRDGOVLGRCEFARICACG 310
 DB 213 YEPVGVSDCTHTNFMCNNSCGMNRPIITITLEDASGKILGRNPEFVRCACG 272
 QY 311 RDRKADEDSIRKQVSDSTKNGDTRKPRFRONTGIDQWTSIKRRSPDELLYLVGRGE 370
 DB 273 RDRTEENFLKKGQSCPEPPPGSTRKALPST-----SSPVOKKKPLDGEYF 329
 QY 371 TYENMLKIKESLELMQVLPQHTIETVRO--QOQOHOHLQKHLISACRNEIVEPRT 428
 DB 330 RFENFRELNALDELKD-----AQTARESGENRAHSHLSK-----KQDS 369
 QY 429 PKQSDVFFRHSKP 441
 DB 370 PS-----RHKKP 376

RESULT 11
 P53_CHICK
 ID P53_CHICK STANDARD: PRT: 367 AA.

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AC P10360;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RC STRAIN=SPAFAS;
RX MEDLINE=89083584; PubMed=3060861;
RA Soussi T.;
RT "Nucleotide sequence of a cDNA encoding the chicken p53 nuclear
RT oncoprotein."
RL Nucleic Acids Res. 16:11383-11383(1988).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND P53 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC -----
CC EMBL; X13057; CA31456.1; -
DR PIR; S02193; S02193.
DR HSSP; P04637; ITR.
DR InterPro; IPR002117; -
DR Pfam; PF00870; P53; 1.
DR PRINTS; PR00386; P53SUPPRESSR.
DR PROSITE; PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation; Apoptosis.
KM DOMAIN 1 30 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 87 278 BY SIMILARITY.
FT DOMAIN 308 339 OLIGOMERIZATION.
FT DOMAIN 347 364 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 292 306 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 366 366 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 367 AA; 40169 MW; FC37D0FCD9F91956 CRC64;

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Query Match 32.1%; Score 764.5; DB 1; Length 367;
Best Local Similarity 44.6%; Pred. No. 1.6e-50;
Matches 169; Conservative 50; Mismatches 105; Indels 55; Gaps 10;

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OY 11 LSP-EVFOHIMDFEOPICSVQPIDLNFVDEPSFDGATNKIEISMDCIRMDSDLSDPMM 69
DB 9 LEPEVEFMDLSMPY---SMQOL-----PLPEDIHNMWELS---PLESPDPPEPP 54
OY 70 PQTNYLGLNLSMDOIOINGSSSTSPYVTDHANSVTAPSPAPQSPFDALSPAPISP 129
DB 55 PPLPL-----AAAAPPLNPP--TPPRAPSPVVEST 85
OY 130 TDYGPSPFSDVSFOQSSSTAKSATWTYTELKKLYCQIAKTCPIQIKVTPPPGAVIRAM 189

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DB 86 EDYGDGDFRVEYVAGTAKSVTCTYSPVLNKVYCRLLAKPCPVYRVNGVAPPGSSILRAV 145
OY 190 PVYKAEHTEVYVRCRPHNELSRFENEGQIAPPSHLIRFEGNSHAOVYEDPTGROSLV 249
DB 146 AVYKSEHVAEVRRCRPHNEKCGGCTDG-LAPAOHLIRVEGNPQARYHDETTKRHSYV 204
OY 250 PYEPPOVTEFTVLYNFMNCSSCVGGMNRRPILLYLETRDGOVLGRRCFEARICACP 309
DB 205 PYEPPEVSGDCTTYLYNFMNCSSCGMNRRLPILLYLETRDGOVLGRRCFEARICACP 264
OY 310 GRDRKADSDIRKOOVSDSTKNGDG--TKRPFONTGSIQMTSIKRRSPDELLYLPVR 367
DB 265 GRDRKIEEENFRK-----RGAGAGVAKRAMSPTEAPEPPK-KRYLNPDEIFYLQVR 316
OY 368 GRETYEMLKIKESLELMQ 386
DB 317 GRRREYEMLKIEALQIAE 335

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RESULT 12
P53_CANFA STANDARD; PRT; 381 AA.
AC Q29537; Q9TV78;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=98178696; PubMed=9519881;
RA Velthoen N., Milner J.;
RT "Isolation of canine p53 cDNA and detailed characterization of the
RT full length canine p53 protein."
RL Oncogene 16:1077-1084(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Setoguchi A., Sakai T., Okuda M., Minehata K., Yazawa M., Ishizaka T.,
RA Wataai T., Hasagawa A., Tsujimoto H.;
RT "Alterations of p53 tumor suppressor gene in various spontaneous
RT tumors in the dog."
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 25-300 FROM N.A.
RC STRAIN=BRAGLE;
RX MEDLINE=95329515; PubMed=7600529;
RA Kraegel S.A., Pazzl K.A., Madewell B.R.;
RT "Sequence analysis of canine p53 in the region of exons 3-8."
RL Cancer Lett. 92:181-186(1995).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND P53 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION.
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
DR EMBL: A060514; AAC16909.1;
DR EMBL: A020761; BAA78379.1;
DR HSSP: S77819; AAB42022.1;
DR InterPro: IPR002117;
DR Pfam: PF00870; P53.1;
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PROSITE: PS00348; P53.1;
KM Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; DNA-binding; Transcription regulation; Apoptosis;
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 89 280 BY SIMILARITY.
FT DOMAIN 313 344 OLIGOMERIZATION.
FT DOMAIN 356 375 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 299 311 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 360 380 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 2 4 BCS -> OEP (IN REF. 2).
FT CONFLICT 378 378 L -> P (IN REF. 2).
SQ SEQUENCE 381 AA: 42486 MW: 761A718FDC93DA59 CRC64;

Query Match 31.68; Score 753.5; DB 1; Length 381;
Best Local Similarity 41.58; Pred. No. 1.2e-49;
Matches 160; Conservative 55; Mismatches 98; Indels 73; Gaps 9;

OY 11 LSPVEVQHINDFL-EOPICSVQ---PID-----INFDERSEDCATNKIEISMDICR 58
DB 14 LSOEFFSELMLDENNVNLSSELCPANDELLPESSVYNWLDSDSDA----- 60
OY 59 MQSDSLSPMPQYTNINGLNSMDQOIONSSSTSPYNTDHAONSVTAPSPYAPSPSTPD 118
DB 61 -----PMRP-----ATSAVTAGP--ASWMLP- 80
OY 119 ALSSPAIPNSNTDYPGPHSPDVSFOQSSSTAKSATWTSTELKKLYCOLAKTCPIQIKWT 178
DB 81 -----SSSVSPKTYPGYGRFLGFLNSGKAKSTWTYSLNLKLLCOLAKTCPIVOLWVS 136
OY 179 PPGQAVIRAMPYKKRAEHTEYVAKRPNHLSREFNEGQIAPSHLIRVEGNSHAQYVE 238
DB 137 PPPPNCVRAALAIYKSEVTEVYVRCRPHERCSDSDG-LAPQHLIRVEGNIRAKYLD 195
OY 239 DPTTGQSVLVPEPQVGTFTTLYNVMCSGVGMNRPIILITVLETRDGOVLGR 298
DB 196 DRTTFHSHVVVYEPPEVSDYTIHYVMCMSSCGMNRPIILITVLETRDSSGNVLR 255
OY 299 RCFEARIACPGDRKADSDIRKQVSDSTKNGDGRKRPRTMTHGIOMSTIKKRSPD 358
DB 256 NSEFVAVACAPDRKRTEENENHKKGECPPPPGSTRFALPST-----SSSPQKKKPLD 312
OY 359 DELLYLVNAGRETYEMLIKESLEL 384
DB 313 GEYFTLOIRGRERYEMFNINLELEL 338

RESULT 13
P53-ORLYA
ID P53-ORLYA STANDARD; PRT; 351 AA.
AC P79820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
GN TP53 OR P53.
OS Oryzias latipes (Medaka fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

CC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
CC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=97305153; PubMed=9161419;
RA Krause M.K., Rhodes L.D., van Beneden R.J.;
RT Cloning of the p53 tumor suppressor gene from the Japanese medaka
RT (Oryzias latipes) and evaluation of mutational hotspots in MNG-
RT exposed fish.
RL Gene 189:101-106(1997).
CC -1- GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND P53 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
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CC or send an email to license@isb-sib.ch).
DR EMBL: U57306; AAC60146.1;
DR HSSP: P04637; LYCS.
DR InterPro: IPR002117;
DR Pfam: PF00870; P53.1;
DR PRINTS: PR00386; P53SUPPRESSOR.
DR PROSITE: PS00348; P53.1;
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; DNA-binding; Transcription regulation; Apoptosis;
FT DOMAIN 1 47 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 86 272 BY SIMILARITY.
FT DOMAIN 301 330 OLIGOMERIZATION.
FT DOMAIN 333 349 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 282 294 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 350 350 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 351 AA: 39666 MW: BC6153363568BEA1 CRC64;

Query Match 31.38; Score 746; DB 1; Length 351;
Best Local Similarity 43.18; Pred. No. 3.8e-49;
Matches 163; Conservative 54; Mismatches 91; Indels 70; Gaps 10;

OY 16 FOHWLDFEOPICGVOPIDINFDERSEDCATNKIEISMDICRMQSDSLSPMPQYTNL 75
DB 14 FOELMETVYPLP---EPLSLPTVNEPTGWSV-----VAGDMFLIDQDLS----- 54
OY 76 GLNSMDQOIONSSSTSPYNTDHAONSVTAPSPYAPSPSTPDALSPSPAIIPNSNTDYPGP 135
DB 55 -----GFDDKI-----FDIP-----IEPVTVNEVNPPTVPTVDYDGS 90
OY 136 HSPDVSFOQSSSTAKSATWTSTELKKLYCOLAKTCPIQIKWTTPPGQAVIRAMPYKKA 195
DB 91 YELFLRQKSGTAKSVTSYSEFLNKLYCOLAKTSPLEVRYSKEPKGAILRAVAVYKKT 150
OY 196 EHTTEVYVRCRPHNELSREFNEGQIAPSHLIRVEGNSHAQYVEDPITGRQSVLVPEPQ 255
DB 151 EHVADVVRCPHND-----NEDSVHRSHLIRVEGNSLAQYFEDPYTKRQSVLVPEPQ 205
OY 256 VGEFTTLYNVMCSGVGMNRPIILITVLETRDGOVLGRRCFARICACPGDRKA 315

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DB 206 PGSEMTTLLSYMCSSCMGMMNRRLITLLET-BGLVLRRCFEVRIACPGDRDKT 264
 QY 316 DESIRKQVSDSKRNGDKTRPRONTHGIOMTSIKRRS-----PDDELLLYLPYRG 368
 DB 265 EESRQKTPK-----KRVYPTMT-----SSKRKSHSGEEDNEVEHFHEVYG 310
 QY 369 RETEMLIKIESLELMQ 386
 DB 311 RERYEFLKINDGELLE 328
 RESULT 14
 P53_BOVIN STANDARD; PRT; 386 AA.
 AC Q29628;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53.
 OS Bos taurus (Bovine), and Bos indicus (Zebu).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_Taxid=9913, 9915;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES-Bovine; TISSUE-Liver;
 RX MEDLINE=95352829; PubMed=7626789;
 RA Dequiedt F., Kettmann R., Burny A., Williams L.;
 RT "Nucleotide sequence of the bovine p53 tumor-suppressor cDNA.";
 RL DNA Seq. 5:261-264(1995).
 RN [2]
 RP SEQUENCE OF 13-386 FROM N.A.
 RC SPECIES-Bovine; STRAIN-HOLSTEIN; TISSUE-Thymus;
 RX MEDLINE=96401400; PubMed=8807776;
 RA Komori H., Ishiguro N., Horiuchi M., Shinagawa M., Aida Y.;
 RT "Predominant p53 mutations in enzootic bovine leukemic cell lines.";
 RL Vet. Immunol. Immunopathol. 52:53-63(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-B. indicus; STRAIN-BORAN; TISSUE-Blood;
 RA Bishop R.R.P., Goblright E.E.I.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
 CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
 CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
 CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION. IS A TRANS-
 CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
 CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
 CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
 CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
 CC BAX AND P45 ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
 CC EXPRESSION.
 CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
 CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
 CC IN MANY TYPES OF CANCER.
 CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
 CC -----
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 CC -----
 CC EMBL: X81704; CA557348.1; -;
 CC EMBL: D49825; BAA08629.1; -;
 CC EMBL: U7486; AAB51214.1; -;
 CC HSSP: P04637; IYCR.

DR InterPro: IP0002117; -;
 DR Pfam: PR00870; P53; 1;
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PROSITE: PS00348; P53; 1.
 KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
 KW Nuclear protein; Phosphorylation; Apoptosis.
 FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
 FT DNA_BIND 94 285 BY SIMILARITY.
 FT DOMAIN 318 349 OLIGOMERIZATION.
 FT DOMAIN 361 380 BASIC (REPRESSION OF DNA-BINDING).
 FT DOMAIN 304 316 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT MOD_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
 FT CONFLICT 380 380 R -> T (IN REF. 2).
 SQ SEQUENCE 386 AA; 43255 MW; 222473F28C548F31 CRC64;
 Query Match 31.1%; Score 741.5; DB 1; Length 386;
 Best Local Similarity 38.4%; Pred. No. 9,4e-49;
 Matches 165; Conservative 68; Mismatches 126; Indels 71; Caps 11;
 QY 11 LSPVEFOHMFLOPQICSVOPIDNPFDESEDAIKIKIEMDCIRMODSLSDPMWP 70
 DB 14 LSOETFSDLWMLPEN-----NLSSLSAPVDD 42
 QY 71 QYTNLGLNLSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPSTFDALSPPA----- 125
 DB 43 LLPYTDVATWIDECNEAPQMPER-----SAPAAPPAT-----PARATSNPL 85
 QY 126 ---IPSNIDYGPSPHFDVSPFOSSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVTPPQ 182
 DB 86 SSFVPSQKTYGNGVFRGLQSGTAKSVCTYSPSLNKLFCQIAKTCPIQVLDWDSPPP 145
 QY 183 GAVIRAMPYRKAEHVEYVKRCRNHELSREFNCGIAPSPHLIRVGNISNAQYVEDPIT 242
 DB 146 GTRVRMAIYKLEHMEYVRCPHERSSDSG-LAPPHLLRVBENLAEYLDQNT 204
 QY 243 GRSVLVYEPPOVGTETFTVLYNPMCNSSCVGGMNRRLITLLETFRDQGVGRCFE 302
 DB 205 FRHSVYVYESPEIDSECTTIHYNFMCNSSCMGMNRRLITLLETLEDSCNLLGRNSFE 264
 QY 303 ARICACPGDRKADSDIRKQVSDSKRNGDKTRPRONTHGIOMTSIKRRSP-DEEL 361
 DB 265 VRVACPGDRDRTEENLRKKGQSCPEPPSTKRALPTNT-----SSSPQKKKPLDGEY 320
 QY 362 LYLVRGRETETMLIKIESLELMQYLPQHITETRYRQOOQH-OHLQKLLS-ACERN 419
 DB 321 FTLDIGRKRYEMRELDALEL-----KDALDREPESSRAHSHLSKRRPSPCHK 375
 QY 420 ELVPPRRREP 429
 DB 376 PML--KREGP 383
 RESULT 15
 P53_MARMO STANDARD; PRT; 391 AA.
 AC Q36006;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE CELLULAR TUMOR ANTIGEN P53 (TUMOR SUPPRESSOR P53).
 GN TP53.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Mammalia.
 OC NCBI_Taxid=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97376996; PubMed=9233767;
 RA Feltelson M.A., Ranganathan P.N., Clayton M.M., Zhang S.M.;
 RT "Partial characterization of the woodchuck tumor suppressor, p53, and
 its interaction with woodchuck hepatitis virus x antigen in

hepatocarcinogenesis.";
RL Oncogene 15:327-336(1997).
CC -1- FUNCTION: ACTS AS A TUMOR SUPPRESSOR IN MANY TUMOR TYPES. INDUCES
CC GROWTH ARREST OR APOPTOSIS DEPENDING ON THE PHYSIOLOGICAL
CC CIRCUMSTANCES OR CELL TYPE, BUT BOTH ACTIVITIES ARE INVOLVED IN
CC TUMOR SUPPRESSION. ACTS IN CELL CYCLE REGULATION, IS A TRANS-
CC ACTIVATOR THAT ACTS TO NEGATIVELY REGULATE CELL DIVISION BY
CC CONTROLLING A SET OF GENES REQUIRED FOR THIS PROCESS. ONE OF THE
CC ACTIVATED GENES IS AN INHIBITOR OF CYCLIN-DEPENDENT KINASES.
CC APOPTOSIS INDUCTION SEEMS TO BE MEDIATED EITHER BY STIMULATION OF
CC BAX AND FAS ANTIGEN EXPRESSION, OR BY REPRESSION OF BCL-2
CC EXPRESSION.
CC -1- SUBUNIT: BINDS DNA AS AN HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DISEASE: P53 IS FOUND IN INCREASED AMOUNTS IN A WIDE VARIETY
CC OF TRANSFORMED CELLS. P53 IS FREQUENTLY MUTATED OR INACTIVATED
CC IN MANY TYPES OF CANCER.
CC -1- SIMILARITY: BELONGS TO THE P53 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ001022; CAA0478.1; -
DR HSSP: P04637; ITR.
DR InterPro: IPR002117; -
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; 1.
KW Anti-oncogene; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein; Phosphorylation.
FT DOMAIN 1 44 TRANSCRIPTION ACTIVATION (ACIDIC).
FT DNA_BIND 100 290 BY SIMILARITY.
FT DOMAIN 323 354 OLIGOMERIZATION.
FT DOMAIN 366 385 BASIC (REPRESSION OF DNA-BINDING).
FT DOMAIN 309 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT MOD_RES 390 390 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 391 AA; 43468 MW; EIDESDBR4BA0182 CRC64;

Query Match 30.9%; Score 736; DB 1; Length 391;
Best Local Similarity 38.0%; Pred. No. 2,5e-48;
Matches 164; Conservative 68; Mismatches 130; Indels 70; Gaps 9;

QY 11 LSPYFQHIWFLQPICSVQPIDLNFVDEPSEDAFNKIEISMDCI RMQSDLSDPMP 70
DB 14 LSOETFSDLWMLP-----ENNVLSPVLS 38
QY 71 QYTNGLNSMDQIIONGSSSTSPYNDHAQNSYAPPAQSPSTFALSPSA----- 125
DB 39 PMDL-LIISFD--VENKFDK---GPEALQMSAAPAPKAPTAPASTLAAPSPATSMPL 91
QY 126 ---IPSNIDYGPSPHSDVSPFOSSSTANSAATWYSTEELKILYQIAKTCPIQIKWTPPQ 182
DB 92 SSVPSQNTYPGVYGFRLGFLHSGTAKSVTCTYSPSLNKLFCQAKTCPVQLWVDSFPP 151
QY 183 GAVIRAMPVYKKAHYEVYKRCNHELSEFNNGQIAPSHLIRVEGNSHAQYVEDPT 242
DB 152 GTRVRAAIAIKKSOHMEVVRCPHNE--RCSDSGLAPQHLIRVEGNLRAEYLD DNT 209
QY 243 GRSVLVPEPPQYGETETVLYNFMCNSSCVGMNRRPILITVLETRDQVYGRCFE 302
DB 210 FRHSVYVPEPEVGSCTIHYNYMCNMSGGMNRRPILITITLEGSSGNLGRNSFE 269
QY 303 ARICACGRDRADEDSIRKQVSDSTKNGDGRPRFRONT-----GIGQTSIKRRSP 357
DB 270 VRVCACGRDRRTDEENFRK-----GEPCEPPPRSTKRALPNGTSSSPQPKKPL 321
QY 358 DDELLIYVKGRETYEMLAKIKESLELMQYLPQHTIETVROQOQOQHLLQKHLISACF 417

DB 322 DGEYTLKIRGAREMFOELNEALDKDAQAEK-----EPGESRPHPSYLSKRGOSTS 376
QY 418 RNELVEPRREP 429
DB 377 RHKKIIFRREGP 388

Search completed: August 8, 2001, 01:42:11
Job time: 390 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 01:36:50 ; Search time 85.05 Seconds
(Without alignments) 696.915 Million cell updates/sec

Title: US-09-670-568b-1

Perfect score: 2383
Sequence: 1 MSQSTQTNFLSPVEVQHIM.....PKQSDVFRHRSKPPNRSVYP 448

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_unclassified:*
14: sp_vertebrate:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2383	100.0	448	4	076078
2	2383	100.0	487	4	09H3D2
3	2296	96.3	483	11	088897
4	2185	91.7	471	4	09NPH7
5	2185	91.7	516	4	09UP27
6	2185	91.7	516	4	09P1B7
7	2185	91.7	555	4	09H3D3
8	2185	91.7	641	4	09UP28
9	2185	91.7	641	4	075195
10	2185	91.7	680	4	09UE10
11	2185	91.7	680	4	09H3D4
12	2169	91.0	555	11	09QW20
13	2169	91.0	680	11	088898
14	2169	91.0	680	11	09JJP6
15	2011	84.4	393	4	075922
16	1938	81.3	389	11	088899
17	1813	76.1	416	4	09P1B6
18	1813	76.1	461	4	09P1B5
19	1813	76.1	461	4	09UP26

20	1813	76.1	586	4	09P1B4	09P1B4 homo sapien
21	1813	76.1	586	4	09UBV9	09UBV9 homo sapien
22	1811	76.0	461	11	09QWY9	09QWY9 mus musculu
23	1811	76.0	586	11	089097	089097 mus musculu
24	1796	75.4	586	4	09UP74	09UP74 homo sapien
25	1796	75.4	586	4	075080	075080 homo sapien
26	1744	73.2	582	13	09DEC7	09dec7 gallus gall
27	1363	57.2	501	4	09H3P8	09h3p8 homo sapien
28	1326.5	55.7	641	13	09W664	09w664 barbus barb
29	1304	54.7	631	11	09JJP2	09jip2 mus musculu
30	1271.5	53.4	590	11	09JJP1	09jip1 mus musculu
31	983	41.3	497	11	09W0J0	09w0j0 mus musculu
32	860.5	36.1	621	5	09NGC7	09ngc7 mya arenari
33	853	35.8	443	5	09NGC8	09ngc8 mya arenari
34	746.5	31.3	352	13	09NSU8	09nsu8 oryzae lat
35	746.5	31.3	352	13	09NSU7	09nsu7 oryzae lat
36	745.5	31.3	364	5	027937	027937 loligo forb
37	735.5	30.9	387	6	09N252	09n252 sus scrofa
38	732.5	30.7	265	13	09W681	09w681 oncorhynch
39	728.5	30.6	265	13	09W682	09w682 oncorhynch
40	725.5	30.4	265	13	09W680	09w680 oncorhynch
41	723.5	30.4	378	14	P89002	P89002 mastomys na
42	717.5	30.1	393	4	09HA08	09haq8 homo sapien
43	716.5	30.1	393	4	016811	016811 homo sapien
44	714	30.0	390	11	070366	070366 mus musculu
45	713.5	29.9	393	4	015087	015087 homo sapien

ALIGNMENTS

RESULT 1
ID 076078 PRELIMINARY: PRT: 448 AA.
AC 076078;
DT 01-NOV-1998 (TRENBLREL. 08, Created)
DT 01-NOV-1998 (TRENBLREL. 08, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE P51 ISOFORM TAP63GAMMA (TA P53 GAMMA).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKeon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKLETAL MUSCLE;
RX MEDLINE=98324755; PubMed=9662378;
RA Osada M., Ohba M., Kawahara C., Ishioka C., Kanamaru R., Katoh I.,
RA Ikawa Y., Nimura Y., Nakagawara A., Ohnata M., Ikawa S.;
RT "Cloning and functional analysis of human p51, which structurally and
RT functionally resembles p53.";
RL Nat. Med. 4:839-843(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tanl M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
DR EMBL: AF075428; AAC62633.1; -;
DR EMBL: AB016072; BAA32592.1; -;
DR EMBL: AF116770; AAF43486.1; -;
DR EMBL: AF116770; AAF43486.1; JOINED.
DR EMBL: AF116756; AAF43486.1; JOINED.
DR EMBL: AF116757; AAF43486.1; JOINED.
DR EMBL: AF116759; AAF43486.1; JOINED.

DR EMBL: AF116760; AAF43486.1; JOINED.
 DR EMBL: AF116761; AAF43486.1; JOINED.
 DR EMBL: AF116762; AAF43486.1; JOINED.
 DR EMBL: AF116763; AAF43486.1; JOINED.
 DR EMBL: AF116764; AAF43486.1; JOINED.
 DR EMBL: AF116765; AAF43486.1; JOINED.
 DR HSSP: P04637; IYCS.
 DR InterPro: IPR002117; -
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; -; 1.
 SO SEQUENCE 448 AA: 50951 MW: A4FF56B8D1E73A6 CRC64;

Query Match 100.0%; Score 2383; DB 4; Length 448;
 Best Local Similarity 100.0%; Pred. No. 8.1e-199;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOTIDLNFVDEPSEDGATNKIEISMDCIRMO 60
 DB 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOTIDLNFVDEPSEDGATNKIEISMDCIRMO 60
 OY 61 DSLSLDPMPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
 DB 61 DSLSLDPMPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
 OY 121 SSPAIPSNITDYPGPHSFVDYFOOSSSTAKATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SSPAIPSNITDYPGPHSFVDYFOOSSSTAKATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180
 OY 181 PGGAIVTAMPYKKAHVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 181 PGGAIVTAMPYKKAHVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 OY 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGANNRPILLIYVLETRDGOVLGRRC 300
 DB 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGANNRPILLIYVLETRDGOVLGRRC 300
 OY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDE 360
 DB 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDE 360
 OY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOOQOQHLLQKHLISACFRNE 420
 DB 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOOQOQHLLQKHLISACFRNE 420
 OY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 DB 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448

RESULT 2
 O9H3D2 PRELIMINARY; PRT; 487 AA.
 AC O9H3D2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 GN TA P63 GAMMA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKoon F.,
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RA Hagihara K., McMenamin M.G., Harris C.C.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF124540; AAG45609.1; -
 DR EMBL: AF124528; AAG45609.1; JOINED.
 DR EMBL: AF124529; AAG45609.1; JOINED.
 DR EMBL: AF124531; AAG45609.1; JOINED.
 DR EMBL: AF124532; AAG45609.1; JOINED.
 DR EMBL: AF124533; AAG45609.1; JOINED.
 DR EMBL: AF124534; AAG45609.1; JOINED.
 DR EMBL: AF124535; AAG45609.1; JOINED.
 SO SEQUENCE 487 AA: 55687 MW: 86C865BDF2643BD CRC64;

Query Match 100.0%; Score 2383; DB 4; Length 487;
 Best Local Similarity 100.0%; Pred. No. 8.9e-199;
 Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOTIDLNFVDEPSEDGATNKIEISMDCIRMO 60
 DB 40 MSOSTQTNELSPVEVFOHIMDFLEOPICSVOTIDLNFVDEPSEDGATNKIEISMDCIRMO 99
 OY 61 DSLSLDPMPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 120
 DB 100 DSLSLDPMPMPQYTNLGLNSMDQOIQNGSSSTSPYNTDHAQNSVTAAPSPSTFDAL 159
 OY 121 SSPAIPSNITDYPGPHSFVDYFOOSSSTAKATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 180
 DB 160 SSPAIPSNITDYPGPHSFVDYFOOSSSTAKATWTYSTEKLKLYCOIAKTCPIQIKVMTTP 219
 OY 181 PGGAIVTAMPYKKAHVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 240
 DB 220 PGGAIVTAMPYKKAHVTEVYKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQYVEDP 279
 OY 241 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGANNRPILLIYVLETRDGOVLGRRC 300
 DB 280 ITGROSVLVPEPPQVGEFTTLYVNFMCNSSCVGANNRPILLIYVLETRDGOVLGRRC 339
 OY 301 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDE 360
 DB 340 FEARICACPGDRKADSDSIRKQVSDSTKNGDGTKRPFRONTHGIOMTSIRKRRSPDE 399
 OY 361 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOOQOQHLLQKHLISACFRNE 420
 DB 400 LLYLPVGRRETYEMILKIKESLELMQYLPQHTIETRYRQOOQOQHLLQKHLISACFRNE 459
 OY 421 LVEPRRETPKQSDVFFRHSKPPNRSVYP 448
 DB 460 LVEPRRETPKQSDVFFRHSKPPNRSVYP 487

RESULT 3
 O88897 PRELIMINARY; PRT; 483 AA.
 AC O88897;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 GN TA-P63 GAMMA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Gillett E., Fleming M.D., Dotsch V., Andrews N.C.,
 RA Caput D., McKoon F.,
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL EMBL: AF075434; AAC62639.1; -
 DR HSSP: P04637; IYCS.

DR InterPro: IPR002117; .
 DR Pfam: PF00870; P53.1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; -.1.
 SO SEQUENCE 483 AA; 54969 MW; A90ED0C110C50EAD CRC64;

Query Match 96.3%; Score 2296; DB 11; Length 483;
 Best Local Similarity 96.9%; Pred. No. 3.2e-191;
 Matches 434; Conservative 3; Mismatches 7; Indels 4; Gaps 1;

QY 1 MSOSTQTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNFDSEDEGATKIKIEMDCIMQ 60
 DB 40 MSOSTQTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNFDSEDEGATKIKIEMDCIMQ 99
 QY 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
 DB 100 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 159
 QY 121 SPSPAIPSNTDYPGPHSFDSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 160 SPSPAIPSNTDYPGPHSFDSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
 QY 181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 DB 220 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 279
 QY 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 280 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 339
 QY 301 FEARICACPGDRKADESIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 360
 DB 340 FEARICACPGDRKADESIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 395
 QY 361 LLYLPVGRRETEYMLKIKESLELMQVLPQHTIETYROOQOQHLOKHLKLSACFNE 420
 DB 396 LLYLPVGRRETEYMLKIKESLELMQVLPQHTIETYROOQOQHLOKHLKLSACFNE 455
 QY 421 LVEPRRETPEKOSDYFFRHSKPPNSVYP 448
 DB 456 LVEPRGEALPTQSDVEFFRHSNPNHSVYP 483

RESULT 4
 Q9NP7 PRELIMINARY; PRT; 471 AA.

AC Q9NP7; TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE P51 ISOFORM TAP63DELTA (P51 DELTA PROTEIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 DR EMBL: AF116771; AAF61624.1; .
 DR EMBL: AF116771; AAF61624.1; .
 DR EMBL: AF116756; AAF43489.1; JOINED.
 DR EMBL: AF116757; AAF43489.1; JOINED.
 DR EMBL: AF116759; AAF43489.1; JOINED.
 DR EMBL: AF116760; AAF43489.1; JOINED.
 DR EMBL: AF116761; AAF43489.1; JOINED.
 DR EMBL: AF116762; AAF43489.1; JOINED.
 DR EMBL: AF116763; AAF43489.1; JOINED.
 DR EMBL: AF116764; AAF43489.1; JOINED.

DR EMBL: AF116765; AAF43489.1; JOINED.
 DR EMBL: AF116766; AAF43489.1; JOINED.
 DR InterPro: IPR002117; .
 DR Pfam: PF00870; P53.1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PROSITE: PS00348; P53; UNKNOWN.1.
 SO SEQUENCE 471 AA; 52882 MW; 32EB39798FCICE69 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 471;
 Best Local Similarity 94.1%; Pred. No. 1.3e-161;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

QY 1 MSOSTQTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNFDSEDEGATKIKIEMDCIMQ 60
 DB 1 MSOSTQTNEFLSPEVFOHIMDFLEOPICSVOPIDLFNFDSEDEGATKIKIEMDCIMQ 60
 QY 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
 DB 61 DSDLSDPMMQPYTNLGLNSMDQIQNGSSSTSPYNTDHAQNSVTAPSPYAPQSSSTFDAL 120
 QY 121 SPSPAIPSNTDYPGPHSFDSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPSNTDYPGPHSFDSFQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 QY 181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 DB 181 POGAVIRAMPYKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVGNSHAQYVEDP 240
 QY 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 DB 241 ITGROSVLVPEPPOVGTETFTVLYNFMCNSSCVGGMNRRPILITVLETRDGOVLGRRC 300
 QY 301 FEARICACPGDRKADESIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 360
 DB 301 FEARICACPGDRKADESIRKQOVSSTKNGDGTGRPFRONTGHIOMTSIKRRSPDE 360
 QY 361 LLYLPVGRRETEYMLKIKESLELMQVLPQHTIETYROOQOQHLOKHLKLSACFNE 420
 DB 361 LLYLPVGRRETEYMLKIKESLELMQVLPQHTIETYROOQOQHLOKHLKLSACFNE 420
 QY 421 LVEPRRETPEKOSDYFFRHSKPP 442
 DB 411 -----QTSIQSPSSYGNSSPP 426

RESULT 5
 Q9UP27 PRELIMINARY; PRT; 516 AA.

AC Q9UP27; TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE TA P63 BETA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kaghad M., Wang Y., Gillette E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKean F.;
 RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 DR EMBL: AF075432; AAC62637.1; .
 DR HSSP: P04637; IYCS
 DR InterPro: IPR002117; .
 DR Pfam: PF00870; P53.1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR PRODOM: PD002681; -.1.
 SO SEQUENCE 516 AA; 57697 MW; 075537810C4738B1 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 516;
 Best Local Similarity 94.1%; Pred. No. 1.5e-181;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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QY 1 MSOSTGTNEFLSEPVQHIWDFLEQICSVOPIDLNFDPESEDEGATKIKIEMDCIRMQ 60
DB 1 MSOSTGTNEFLSEPVQHIWDFLEQICSVOPIDLNFDPESEDEGATKIKIEMDCIRMQ 60
QY 61 DSDLSPPMPQYNTNGLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLSPPMPQYNTNGLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFQVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVTPP 180
DB 121 SPSPAIPSNTDYPGPHSFQVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVTPP 180
QY 181 PGCAVIIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQVYEDP 240
DB 181 PGCAVIIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQVYEDP 240
QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCGVGMNRRPILITVLETRDQVIGRRRC 300
DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCGVGMNRRPILITVLETRDQVIGRRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPRFQNTHGLOMTSIRKRRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPRFQNTHGLOMTSIRKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETFRQOQOQOHLLQKHLISACFRNE 420
DB 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETFRQOQOQOHLLQKHLISACFRNE 420
QY 421 LVEPRRETPKOSDVEFRHSKRP 442
DB 411 -----QTSIQSPSSSTGNSSPP 426

RESULT 6
Q9P1B7 PRELIMINARY: PRT: 516 AA.
AC 09P1B7:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
P51 ISOFORM TAP63BETA.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20388515; PubMed=10935472;
RA Tanai M., Shimizu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RT Neoplasia 1:71-79(1999).
DR EMBL: AF116768; AAF43488.1; JOINED.
DR EMBL: AF116756; AAF43488.1; JOINED.
DR EMBL: AF116757; AAF43488.1; JOINED.
DR EMBL: AF116760; AAF43488.1; JOINED.
DR EMBL: AF116769; AAF43488.1; JOINED.
DR EMBL: AF116761; AAF43488.1; JOINED.
DR EMBL: AF116762; AAF43488.1; JOINED.
DR EMBL: AF116763; AAF43488.1; JOINED.
DR EMBL: AF116764; AAF43488.1; JOINED.
DR EMBL: AF116765; AAF43488.1; JOINED.
DR EMBL: AF116766; AAF43488.1; JOINED.
DR EMBL: AF116767; AAF43488.1; JOINED.
DR InterPro: IPR002117; -.
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.

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DR PROSITE: PS00348; P53; UNKNOWN_1.
 SO SEQUENCE 516 AA; 57598 MW; 07553781103738B1 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 516;
 Best Local Similarity 94.1%; Pred. No. 1.5e-181;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

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QY 1 MSOSTGTNEFLSEPVQHIWDFLEQICSVOPIDLNFDPESEDEGATKIKIEMDCIRMQ 60
DB 1 MSOSTGTNEFLSEPVQHIWDFLEQICSVOPIDLNFDPESEDEGATKIKIEMDCIRMQ 60
QY 61 DSDLSPPMPQYNTNGLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPAQPSSTFDAL 120
DB 61 DSDLSPPMPQYNTNGLNSMDQIQNGSSSTPYNTDHAQNSVTAPSPAQPSSTFDAL 120
QY 121 SPSPAIPSNTDYPGPHSFQVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVTPP 180
DB 121 SPSPAIPSNTDYPGPHSFQVDFVFOQSSSTAKSATWTYSTELKLYCOIAKTCPIQIKVTPP 180
QY 181 PGCAVIIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQVYEDP 240
DB 181 PGCAVIIRAMPYVKKAEHTEVVKRCPNHELSEFNEGOIAPPSHLIRVEGNSHAQVYEDP 240
QY 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCGVGMNRRPILITVLETRDQVIGRRRC 300
DB 241 ITGRQSVLVPEPPOVGTETFTVLYNFCNSSCGVGMNRRPILITVLETRDQVIGRRRC 300
QY 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPRFQNTHGLOMTSIRKRRSPDDE 360
DB 301 FEARICACPGDRKRADEDSIRKQOVSDSTKNGDKTRKPRFQNTHGLOMTSIRKRRSPDDE 360
QY 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETFRQOQOQOHLLQKHLISACFRNE 420
DB 361 LLYLPVGRRETYEMLLIKESLELMQYLPQHTIETFRQOQOQOHLLQKHLISACFRNE 420
QY 421 LVEPRRETPKOSDVEFRHSKRP 442
DB 411 -----QTSIQSPSSSTGNSSPP 426

RESULT 7
Q9H3D3 PRELIMINARY: PRT: 555 AA.
AC 09H3D3:
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
TA P63 BETA.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98448095; PubMed=9774969;
RA Yang A., Kaghad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
RA Andrews N.C., Caput D., McKoon F.;
RT "p63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RT Mol. Cell 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Hagihara K., McMenamin M.G., Harris C.C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF124529; AAG45608.1; JOINED.
DR EMBL: AF124528; AAG45608.1; JOINED.
DR EMBL: AF124529; AAG45608.1; JOINED.
DR EMBL: AF124531; AAG45608.1; JOINED.
DR EMBL: AF124532; AAG45608.1; JOINED.
DR EMBL: AF124533; AAG45608.1; JOINED.
DR EMBL: AF124534; AAG45608.1; JOINED.

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DR EMBL: AF124535; AAC45608.1; JOINED.
 DR EMBL: AF124536; AAC45608.1; JOINED.
 DR EMBL: AF124537; AAC45608.1; JOINED.
 SO SEQUENCE 555 AA: 62433 MW: E22874BE7DBABCB CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 555;
 Best Local Similarity 94.1%; Pred. No. 1.6e-181;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

OY 1 MSOSTQTNEFLSPEVFGHIMDFLEOPICSVOPIDLFNVEPSESDGATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPEVFGHIMDFLEOPICSVOPIDLFNVEPSESDGATNKIEISMDCIRMQ 99
 OY 61 DSDLDPMWPOYTNGILNSMDQOIONGSSSTSPYNTHAONSVTAPSPYAPQSPSTFDAL 120
 DB 100 DSDLDPMWPOYTNGILNSMDQOIONGSSSTSPYNTHAONSVTAPSPYAPQSPSTFDAL 159
 OY 121 SPSPAIPNTDYPGPHSPDVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 160 SPSPAIPNTDYPGPHSPDVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 219
 OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDP 240
 DB 220 POGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDP 279
 OY 241 ITGRQSVLVPEPPOVGEFTTTLVLYNFMCNSSCVGAMRRPILIVTLETROGOVLGRRC 300
 DB 280 ITGRQSVLVPEPPOVGEFTTTLVLYNFMCNSSCVGAMRRPILIVTLETROGOVLGRRC 339
 OY 301 FEARICACPGDRKRADESIKROQVSDSTKNGDGTKRPFRONTGHIQMTSIKRRSPDE 360
 DB 340 FEARICACPGDRKRADESIKROQVSDSTKNGDGTKRPFRONTGHIQMTSIKRRSPDE 399
 OY 361 LLYLPVRCRETYEMLLKIKESLELMQVLPQHTIETTYROOQOOHOLLKILLSACFENE 420
 DB 400 LLYLPVRCRETYEMLLKIKESLELMQVLPQHTIETTYROOQOOHOLLKILLSACFENE 449
 OY 421 LVEPRRETPTKOSDVFRHSKRP 442
 DB 450 -----QTSIOSPSSTYGNSSPP 465

RESULT 8
 ID 09UP28 PRELIMINARY: PRT: 641 AA.
 AC 09UP28;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE TA P63 ALPHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=98448095; PubMed=9774969;
 RA Yang A., Kagnad M., Wang Y., Gillett E., Fleming M.D., Dotsch V.,
 RA Andrews N.C., Caput D., McKeon F.;
 RT "p53, a p53 homolog at 3q27-29, encodes multiple products with
 RT transactivating, death-inducing, and dominant-negative activities.";
 RL Mol. Cell 2:305-316(1998).
 DR EMBL: AF075430; AAC62635.1; -
 DR HSSP: P04637; IYCS.
 DR InterPro: IPR001660; -
 DR InterPro: IPR002117; -
 DR Pfam: PF00870; P53; 1.
 DR PRINTS: PR00386; P53SUPPRESSR.
 DR SMART: SM00454; SAM; 1.
 SO SEQUENCE 641 AA: 72049 MW: 23A25EBAE63F605 CRC64;

Query Match 91.7%; Score 2185; DB 4; Length 641;
 Best Local Similarity 94.1%; Pred. No. 2e-181;
 Matches 416; Conservative 3; Mismatches 7; Indels 16; Gaps 1;

OY 1 MSOSTQTNEFLSPEVFGHIMDFLEOPICSVOPIDLFNVEPSESDGATNKIEISMDCIRMQ 60
 DB 1 MSOSTQTNEFLSPEVFGHIMDFLEOPICSVOPIDLFNVEPSESDGATNKIEISMDCIRMQ 60
 OY 61 DSDLDPMWPOYTNGILNSMDQOIONGSSSTSPYNTHAONSVTAPSPYAPQSPSTFDAL 120
 DB 61 DSDLDPMWPOYTNGILNSMDQOIONGSSSTSPYNTHAONSVTAPSPYAPQSPSTFDAL 120
 OY 121 SPSPAIPNTDYPGPHSPDVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 DB 121 SPSPAIPNTDYPGPHSPDVFSQOSTAKSATWTYSTELKLYCOIAKTCPIQIKVMTTP 180
 OY 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDP 240
 DB 181 POGAVIRAMPYKKAHEVTEVVKRCPNHELRENEGQIAPPSHLIRVEGNSHAQYEDP 240
 OY 241 ITGRQSVLVPEPPOVGEFTTTLVLYNFMCNSSCVGAMRRPILIVTLETROGOVLGRRC 300
 DB 241 ITGRQSVLVPEPPOVGEFTTTLVLYNFMCNSSCVGAMRRPILIVTLETROGOVLGRRC 300
 OY 301 FEARICACPGDRKRADESIKROQVSDSTKNGDGTKRPFRONTGHIQMTSIKRRSPDE 360
 DB 301 FEARICACPGDRKRADESIKROQVSDSTKNGDGTKRPFRONTGHIQMTSIKRRSPDE 360
 OY 361 LLYLPVRCRETYEMLLKIKESLELMQVLPQHTIETTYROOQOOHOLLKILLSACFENE 420
 DB 361 LLYLPVRCRETYEMLLKIKESLELMQVLPQHTIETTYROOQOOHOLLKILLSACFENE 410
 OY 421 LVEPRRETPTKOSDVFRHSKRP 442
 DB 441 -----QTSIOSPSSTYGNSSPP 426

RESULT 9
 ID 075195 PRELIMINARY: PRT: 641 AA.
 AC 075195;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE P51 ISOFORM TAP63ALPHA (P51B PROTEIN).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC TISSUE=SKETETAL MUSCLE;
 RX MEDLINE=98324755; PubMed=9662378;
 RA Osada M., Ohba M., Kawahara C., Ishioke C., Kanamaru R., Katoh I.,
 RA Ikawa Y., Nimura Y., Nakagawara A., Obinata M.;
 RT "Cloning and functional analysis of human p51, which structurally and
 RT functionally resembles p53.";
 RL Nat. Med. 4:839-844(1998).
 RN [2]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=20388515; PubMed=10935472;
 RA Tanli M., Shindzu K., Kawahara C., Kohno T., Ishimoto O., Ikawa S.,
 RA Yokota J.;
 RT "Mutation and expression of the p51 gene in human lung cancer.";
 RL Neoplasia 1:71-79(1999).
 DR EMBL: AB016073; BAA32593.1; -
 DR EMBL: AF116769; AAF43487.1; -
 DR EMBL: AF116756; AAF43487.1; JOINED.
 DR EMBL: AF116757; AAF43487.1; JOINED.
 DR EMBL: AF116759; AAF43487.1; JOINED.
 DR EMBL: AF116760; AAF43487.1; JOINED.
 DR EMBL: AF116761; AAF43487.1; JOINED.
 DR EMBL: AF116762; AAF43487.1; JOINED.


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Query Match          91.0%; Score 2169; DB 11; Length 680;
Best Local Similarity 93.2%; Pred. No. 5,2e-180;
Matches 412; Conservative 6; Mismatches 8; Indels 16; Gaps 1;

OY 1 MSOSTQTNFEFLSPVEFHQIHWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMO 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 MSOSTQTSSEFLSPVEFHQIHWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMO 99
OY 61 DSDLDSPMPPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSSSTFDAL 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 100 DSDLDSPMPPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSSSTFDAL 159
OY 121 SPSPAIIPSNITDVPGRHSPDVSPFOSSSTAKSATWTYSTELKTKLYCOIAKTCPIQIKWMP 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 160 SPSPAIIPSNITDVPGRHSPDVSPFOSSSTAKSATWTYSTELKTKLYCOIAKTCPIQIKWMP 219
OY 181 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 PGCAVIRAMPYVKKAEHTEVYKRCPNHLSREFNEGOIAPSHLIRVEGNSHAQYVEDP 279
OY 241 ITGRQSVLVPEPPQVGTFTTYLYNFMCNSSCVGGMRRPILITVLTETRDGQVLRRC 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 ITGRQSVLVPEPPQVGTFTTYLYNFMCNSSCVGGMRRPILITVLTETRDGQVLRRC 339
OY 301 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDE 360
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 340 FEARICACGPRDKADEDSIRKQOVSSTKNGDGTKRPRFRONTGHIOMTSIKRRSPDDE 399
OY 361 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYROOQOQOHLLOKHLISACFRNE 420
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 400 LLYLPVRGRETEYMLTKIKESLELMQYLPQHTIETRYROOQOQOHLLOKHLISACFRNE 449
OY 421 LVEPRERETPKOSDVFFRHSKPP 442
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 450 -----QTSMSQSSSYGNSSPP 465

RESULT 14
O9JUP6 PRELIMINARY; PRT; 680 AA.
AC O9JUP6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TA2 KET ALPHA.
GN P63.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LINGUAL EPITHELIUM;
RA MEDLINE=97460723; Pubmed=9115105;
RT Schmale H., Bamberger C.;
RT "A novel protein with strong homology to the tumor suppressor p53.";
RL Oncogene 15:1363-1367(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LINGUAL EPITHELIUM;
RA Schmale H.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y10258; CAB8216.1; -
DR InterPro: IPR002117; -
DR Pfam: PF00870; P53; 1.
DR PRINTS: PR00386; P53SUPPRESSR.
DR PROSITE: PS00348; P53; UNKNOWN.1.
SQ SEQUENCE 680 AA; 76760 MW; AC45DABB88F61400 CRC64;

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OY 1 MSOSTQTNFEFLSPVEFHQIHWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMO 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 MSOSTQTSSEFLSPVEFHQIHWDFLEQPICSVOPIDLNFDVDESEDGATNKIETSMDCIRMO 99
OY 61 DSDLDSPMPPOYTNTGLNSMDQOIONGSSSTSPYNTDHAONSVTAPSPYAOPSSSTFDAL 120
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DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
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RA Yang A., Kaghad M., Gallet E., Fleming M.D., Dotsch V., Andrews N.C.,
RA Caput D., McKoon F.;
RT "P63, a p53 homolog at 3q27-29, encodes multiple products with
RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
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RP SEQUENCE FROM N.A.
RC MEDLINE=20388515; Pubmed=10935472;
RA Tani M., Shimizu K., Kawahara C., Kohno T., Ishimoco O., Ikawa S.,
RA Yokota J.;
RT "Mutation and expression of the p51 gene in human lung cancer.";
RL Neoplasia 1:71-79(1999).
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RA Andrews N.C., Caput D., McKoon F.;
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RT transactivating, death-inducing, and dominant-negative activities.";
RL Mol. Cell 2:305-316(1998).
RN [4]
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RC Hagihara K., McMenamin M.G., Harris C.C.;

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RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 21:23:00 ; Search time 4864.29 Seconds
(Without alignments)
8954.479 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2688314

Minimum DB seg length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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96: gb_pi12:*
97: gb_pi13:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1364	48.4	4846	9	AX009538	AX009538 Sequence
6	1364	48.4	4849	92	HS016961	Y16961 Homo sapien
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ACCESSION AF116770
VERSION AF116770.1 GI:7248444

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AUTHORS Tan, M., Shimizu, K., Kawahara, C., Kohno, T., Ishimoto, O., Ikawa, S. and Yokota, J.
TITLE Mutation and expression of the p51 gene in human lung cancer
JOURNAL Neoplasia 1 (1), 71-79 (1999)
MEDLINE 20388515
AUTHORS 2 (bases 1 to 1516)
TITLE Tan, M., Shimizu, K., Kohno, T., Ikawa, S. and Yokota, J.
JOURNAL Direct Submission
REFERENCE Submitted (28-DEC-1998) Biology Division, National Cancer Center Research Institute, 1-1. Tsukiji 5-chome, Chuo-Ku, Tokyo 104-0045, Japan
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exon
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RESULT 3
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LOCUS Homo sapiens p51 delta mRNA, complete cds.
DEFINITION AF116771
ACCESSION AF116771.1 GI:7384975
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2031)
AUTHORS Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.
TITLE Mutations and expression of the p51 gene in human lung cancer
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2031)
AUTHORS Tani,M., Shimizu,K., Kohno,T., Ikawa,S. and Yokota,J.
TITLE Direct Submission
JOURNAL Submitted (28-DEC-1998) Biology Division, National Cancer Center Research Institute, 1-1, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan

FEATURES
Source location/qualifiers
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DEFINITION Homo sapiens mRNA for p51b, complete cds.
ACCESSION AB016073
VERSION AB016073.1 GI:3510329
KEYWORDS p51b.
SOURCE Homo sapiens
ORGANISM Homo sapiens skeletal muscle cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2270)
AUTHORS Ikawa, S. and Osada, M.
JOURNAL Direct Submission
TITLE Submitted (10-JUL-1998) to the DBJ/EMBL/GenBank databases.
AUTHORS Shuntaro Ikawa, Institute of Development, Aging and Cancer,
DEPARTMENT Department of Cell Biology; 4-1 Setryo-machi, Sendai, Miyagi
JOURNAL Tel:81-22-717-8484, Fax:81-22-717-8488)
REFERENCE 2 (sites)
AUTHORS Osada, M., Ohba, M., Kawahara, C., Ishioke, C., Kanamaru, R., Katoh, I.,
TITLE Ikawa, T., Nlmura, Y., Nakagawara, A., Obinata, M. and Ikawa, S.
JOURNAL Cloning and functional analysis of human p51, which structurally
MEDLINE and functionally resembles p53
FEATURES
SOURCE Nat. Med. 4 (7), 839-843 (1998)
98324755
location/Qualifiers
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ACCESSION AX009538
VERSION AX009538.1 GI:9996812
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 4846)
AUTHORS Bamberg, C., Paul, D., Augustin, M. and Schmale, H.
TITLE Tumour suppressor genes of the p53 family
JOURNAL Patent: WO 9961610-A.2 02-DEC-1999;
BAMBERGER CASIMIR (DE); PAUL DIETER (DE); AUGUSTIN MARTIN (DE);
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RESULT 10
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ACCESSION AF075434.1 GI:3695089
VERSION
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SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Yang, A., Kaghad, M., Wang, Y., Gillett, E., Fleming, M.D., Dotsch, V.,
1 (bases 1 to 1452)
p53, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 505-516 (1998)
JOURNAL
MEDLINE 98448095
REFERENCE 2 (bases 1 to 1452)
AUTHORS Yang, A., Kaghad, M., Caput, D. and McKeon, F.
TITLE Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
JOURNAL Longwood Ave, Boston, MA 02115, USA
FEATURES
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1. 1452
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BASE COUNT 394 a 427 c 341 g 290 t
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Best Local Similarity 90.6%; Pred. No. 1.7e-286;
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LOCUS Rsetus norvegicus mRNA for Taz2 KET alpha protein (p63 gene).
DEFINITION Y10258
VERSION Y10258.2 GI:7630116
KEYWORDS p63 gene; Taz2 KET alpha protein.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 4991)
AUTHORS Schmale, H. and Bamberger, C.
TITLE A novel protein with strong homology to the tumor suppressor p53
JOURNAL Oncogene 15 (11), 1363-1367 (1997)
MEDLINE 97460723
REFERENCE 2 (bases 1 to 4991)
AUTHORS Schmale, H.
TITLE Direct Submission
JOURNAL Submitted (23-DEC-1996) H. Schmale, Institut fuer Zellbiochemie und
Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf,
Martinistrasse 52, D-20246 Hamburg, FRG
REMARK 3 (bases 1 to 4991)
AUTHORS Schmale, H.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2000) H. Schmale, Institut fuer Zellbiochemie und
Klinische Neurobiologie, Universitaetskrankenhaus Eppendorf,
Martinistrasse 52, D-20246 Hamburg, FRG
COMMENT On Apr 20, 2000 this sequence version replaced gi:2437846.
FEATURES
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ORIGIN

Query Match 41.4%; Score 1166.2; DB 95; Length 4991;
Best Local Similarity 91.0%; Pred. No. 1.9e-273;
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QY 182 cagaagtttccagacataltggaatttctgaaacagcctalatgttcaagtcacca 241
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DB 422 GCATGGATTGTATCCGATGCAAGACCTGACCTCAGTACCCCATGTGGCCACAGTACA 481
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LOCUS	AF075435 1668 bp mRNA 04-OCT-1998
DEFINITION	Mus musculus TA*p63 beta mRNA, complete cds.
ACCESSION	AF075435
VERSION	AF075435.1 GI:3695091
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 1668)
AUTHORS	Yang, A., Kagnad, M., Wang, Y., Gillette, E., Fleming, M.D., Dotsch, V., Andrews, N.C., Caput, D. and McKee, F.
TITLE	p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities
JOURNAL	Mol. Cell 2 (3), 305-316 (1998)
FEATURES	<p>2 (bases 1 to 1668)</p> <p>98448095</p> <p>Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA</p> <p>Location/Qualifiers</p> <p>1..1668</p> <p>/organism="Mus musculus"</p> <p>/db_xref="taxon:10090"</p> <p>/chromosome="16"</p>
CDs	<p>1. 1668</p> <p>/function="transcription factor"</p> <p>/note="second splice variant; related to p53 and p73"</p> <p>/product_start=1</p> <p>/product="TA*p63 beta"</p> <p>/protein_id="AAC62640.1"</p> <p>/db_xref="GI:3695092"</p> <p>/translation="MNFETSRCATLOVCPPDYIOFLETPAHFSKESYRSAMSOSTGRSEPEVPOHIDPLFEPICSVOPLELNFVDEPSENGATNKEIETSMDCIRKDDSLSDPMPROPTINGLISMDMOONSSSTPYNDHONSTVAPSPASPTDVPSPGAVTSNTDYPGHSFDEFSFOOSTASATWYSTETKLYCIATCPQIKRVPPEPAGVTRAMPYVKKRAHEVTEVYKRCRPHNELSRPNEQIAPSHLIRVENSIAQVYEDPTGROSLVLYEPEPOVGETTVLVNFMNSSCVGANNRRLILIYLETEDQVLPGRFCGRIACAPGRDKADEDSIRKOOVSASANGDGTAPRPRONHG10MTSIRKTSQSDDELLYLVEVGRETEYEMLKIKESILETMOYLPQHTIETVROQOOQOHLOKQRTSQQSSYSGNSPPLNKENSNNKLPSPYSOLINPOORALPTPTMPEGMANIMMCTHMMADNMGLNSTPTLOLPLPLSPMPSHCTPPPPYPTDCSIVRIIMOV"</p>
BASE COUNT	451 a 512 c 380 g 325 t
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OY	868	acagagaagacagagtgtgctgttaacctataagccaccccaagtttgacatgaattcacg	927
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RESULT 13
AF075436
LOCUS AF075436 2043 bp mRNA ROD 04-OCT-1998
DEFINITION Mus musculus TA-p63 alpha mRNA, complete cds.
ACCESSION AF075436
KEYWORDS AF075436.1 GI:3695093
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 2043)
AUTHORS Yang, A., Kaghad, M., Wang, Y., Gilllett, E., Fleming, M.D., Dotson, V.,
Andrews, N.C., Caput, D. and McKee, F.
p63, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
98448095

TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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1. 2043
/organism="Mus musculus"
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1. 2043
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Oy 89 cgttctgtagaaa-ccagatcattctctcttggaaaagaagtattacagatccacatg 147
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Db 61 CGTTTCATGAAACCCCAAGCTCATTTCTGTGGAAGAAGATATTACAGATCTGCATG 120
Oy 148 tcccaagacacacagacaaatgaattctcagtcagagaggtttccagatctcggat 207
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Db 121 TCGCAGAGCACCACAGCAAGCAGATTCTCAGCCAGAGAGGTCTTCACCATATCTGGGAT 180
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Oy 268 tcagaagaatggtgcgacaaacaagaatgaatgaatgaatgaatgaatgaatgaatga 327
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Oy 388 gacacagcagatcagaagcgtcctcgtccacagctccctataacaagaacacagcag 447
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Db 361 GACACGACATTCAGACAGCGCTCTCTGTCACACAGCCCTTAAACACAGACACGACAG 420
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DEFINITION	AF075429	AF075429.1	GI:3695079
VERSION	AF075429.1	GI:3695079	
KEYWORDS		human.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 1182)	
JOURNAL		Yang, A., Kaghad, M., Wang, Y., Gillette, E., Fleming, M.D., Dotsch, V.,	
MEDLINE		Andrews, N.C., Caput, D. and McKeon, F.	
REFERENCE		p53, a p53 homolog at 3q27.2, encodes multiple products with	
AUTHORS		transactivating, death-inducing, and dominant-negative activities	
TITLE		Mol. Cell 2 (3), 305-316 (1998)	
JOURNAL		2 (bases 1 to 1182)	
MEDLINE		Yang, A., Kaghad, M., Caput, D. and McKeon, F.	
REFERENCE		Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240	
AUTHORS		Longwood Ave, Boston, MA 02115, USA	
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BASE COUNT	330 a	342 c	276 g 234 t
ORIGIN			

Query Match	Best Local Similarity	40.6%	Score 1143.6:	DB 88:	Length 1182:
Matches 1155:	Conservative	0:	Mismatches 19:	Indels	Gaps
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Qy 378	gaacacagatgagccagacagatttcgaaagcgctctgtccacacagctccctataacacaga	437			
Db 69	GAACAGATGAGCAACACAGATTTCAAAAGCGCTCTCTGTCACACAGTCCCTATTACACAGA	128			
Qy 438	ccacgcgcagaacagcagtcacgcgcgcctctgcacctacgcacagccagctccaccttcga	497			
Db 129	CCACGCCCAAAAGAGGTGACGGGGCCCTCGGCCGCTACGACAGGCCAGCTCCACTTTCGA	188			
Qy 498	tgcctctctccatcaaccgcacatccctcccaacacacgagatcacccagagcccgagagatt	557			
Db 189	TGCTCTCTCTCCATCCACCCGCTATCCCTCCCAACACGCACTACCCAGGCCCGACAGTTT	248			
Qy 558	cgaagctctccctcagacagtcagacacgcgcgaagtcgcgcacccctgcagctatccacatga	617			
Db 249	CGAGGTGTCTTCCAGCATGTCCAGCACCCGCAAGTGGGCCACGTGGACGTATTCCACTGA	308			
Qy 618	actgaagaactctactctgccaatctgcaaaagacatgcccacatccagatcaagttgatgac	677			
Db 309	ACTGAAGAACTCTACTGCGCAATTTCAAGACATGCCCCATCCAGATCAACAGGTGATGAC	368			
Qy 678	cccaactctccagagagctgcttaccggccatgctctcttcaaaaaagctatgacagct	737			
Db 369	CCCACTCTCTCAGGAGACTCTTATCCGGCCCATGCTGTCTTCAAAAAAGCTGACACGT	428			
Qy 738	cacgcagatgtgtgaagcgcgtgcccacacatgagcttgagccgtgaattcaacagagggaca	797			
Db 429	CACGAGGTGGTGAAGGGGTGCCCAACCATGAGCTGAGCGGTGAATTCACAGGGGACA	488			
Qy 798	gattgccccctcattgatttgagtgagtgaggggaacagccatgcccagctatgaga	857			
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Db 549	AATTCCTCATCAGAGAGACAGAGTGTGCTTATGAGCCACCCAGCTGTGGCAC	608			
Qy 918	tgaattcagacagctctgttacaattcattgattgatacagcagctgtgttgaggagatgaa	977			
Db 609	TGAATTTACAGCAGCTTGTTCATATTTTCATAGTGTACACCACTTGTGTGAGGGATGAA	668			
Qy 978	cgcgcgtccaatttlaatcatctgttactctcgtgaacccaagatacggcagctccgggcg	1037			
Db 669	CCGCGCTCAATTTTAACTATTGTTACTCTGGAACACAGATGGGCAAGTCTGGGGCG	728			
Qy 1038	acgctgctcttgagcccgatctgtgcttgcccaggaagacagaaagcgagatgaa	1097			
Db 729	ACGCTGCTTTGAGGCCCGGATCTGTGCTTCCAGAGAAAGACAGAGAGCGCGATGAAGA	788			
Qy 1098	tagcatcagaaagcagcaagcttcctgcgcagtaacaaagacgctgtgtgtgacaaagcgcc	1157			
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Db 849	GTTTCTCTCAAAACACATGATGTATCTCCAGATGACATCTCATCAAGAAACGAAGATCCCGA	908			
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Db 969	CAAAAGTCTCCCTGGAACTCATATCACTACTCTTCTCACACACATTTGAACCTACAGGCA	1028			

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 22:04:29 ; Search time 221.11 Seconds
(without alignments)
7996.793 Million cell updates/sec

Title: US-09-670-568B-2

Perfect score: 2816
Sequence: 1 tgcctgatatcaagaacagt.....gcattctgttgtaaaagaaa 2816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2816	100.0	2816	20	AAZ25770	Human p51 encoding
2	2816	100.0	2816	21	AAZ25770	Human lung cancer
3	1376	48.9	2270	20	AAZ25771	Human p51 encoding
4	1376	48.9	2270	21	AAZ25771	Human lung cancer
5	1364	48.4	4846	21	AAZ43913	Human KET CDNA. H
6	1364	48.4	4849	21	AAZ43913	Human lung cancer
7	1346	47.8	1347	20	AAZ58574	Human cell regulat
8	1232	43.8	1551	20	AAZ58573	Human cell regulat
9	1232	43.8	1551	21	AAZ58573	Human lung cancer
10	1232	43.8	1926	20	AAZ58572	Human cell regulat
11	1218.2	43.3	1452	20	AAZ58580	Mouse cell regulat

12	1154.6	41.0	2043	20	AAZ58577	Human cell regulat
13	1143.6	40.6	1182	20	AAZ58576	Human cell regulat
14	1031.2	36.6	2082	20	AAZ27674	Human p40 coding s
15	1031.2	36.6	2082	21	AAZ27674	Human lung cancer
16	1031.2	36.6	2082	21	AAZ27674	Rat KET CDNA. Rat
17	1028.6	36.5	1386	21	AAZ43912	Human lung cancer
18	1028.6	36.5	1386	21	AAZ43912	Human cell regulat
19	1027.6	36.5	1655	21	AAZ58575	Human lung cancer
20	1026.4	36.4	2820	21	AAZ58575	Human lung cancer
21	951.2	33.8	1170	20	AAZ58583	Human cell regulat
22	922.8	32.8	4643	20	AAZ24648	Human lung tumor a
23	884.6	31.4	1386	20	AAZ58582	Mouse cell regulat
24	884.6	31.4	1761	20	AAZ58581	Mouse cell regulat
25	466.8	16.6	1594	21	AAZ49690	Human p73 protein
26	466.8	16.6	1817	18	AAZ58580	Human p53 tumour s
27	466.8	16.6	1870	18	AAZ58581	Human p53 tumour s
28	466.8	16.6	2156	18	AAZ58582	Human p53 tumour s
29	466.4	16.6	1521	18	AAZ58583	Human p53 tumour s
30	466.4	16.6	1764	18	AAZ58584	Human p53 tumour s
31	463.8	16.5	2034	18	AAZ58585	Human p53 tumour s
32	463.8	16.5	2874	18	AAZ58586	Human p53 tumour s
33	458.6	16.3	2040	18	AAZ58587	Human p53 tumour s
34	308	10.9	308	22	AAZ58588	Human p53 tumour s
35	244.2	8.7	1215	17	AAZ58589	Human p53 tumour s
36	244.2	8.6	1181	16	AAZ58590	Human p53 tumour s
37	242.6	8.6	1181	20	AAZ58591	Human p53 tumour s
38	242.6	8.6	1181	21	AAZ58592	Human p53 tumour s
39	242.6	8.6	1181	21	AAZ58593	Human p53 tumour s
40	242.6	8.6	1182	15	AAZ58594	Human p53 tumour s
41	242.6	8.6	1182	17	AAZ58595	Human p53 tumour s
42	242.6	8.6	1182	20	AAZ58596	Human p53 tumour s
43	242.6	8.6	1182	17	AAZ58597	Human p53 tumour s
44	242.6	8.6	1203	17	AAZ58598	Human p53 tumour s
45	242.6	8.6	1209	18	AAZ58599	Human p53 tumour s

ALIGNMENTS

RESULT 1	
AAZ25770	AAZ25770 standard; CDNA: 2816 BP.
AAZ25770;	
07-JAN-2000	(first entry)
Human p51 encoding	CDNA A.
Human; p51; p53 related gene; cell proliferation; regulation; cancer;	
tumour suppression; diagnosis; ss.	
Homo sapiens.	
Key	Location/Qualifiers
CDS	145..1491
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FT	2786..2791
FT	/*tag=b
W09950412-A1.	
07-OCT-1999.	
24-MAR-1999;	99WO-JP01512.
27-MAR-1998;	98JP-0100467.
(SAKA) OTSUKA PHARM CO LTD.	
(IKAWA) IKAWA Y.	
Ikawa Y, Ikawa S, Obinata M;	

Db 2461 ctgatactgttcagtgactttagccagagacttactgttttagtaagtgagatccaagc 2520
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RESULT 3

AA25771
ID AA25771 standard; CDNA: 2270 BP.

XX AC AA25771:

XX DT 07-JAN-2000 (first entry)

XX DE Human p51 encoding cDNA B.

XX KW Human; p51; p53 related gene; cell proliferation; regulation; cancer;

XX KH tumour suppression; diagnosis; ss.

XX OS Homo sapiens.

XX FH Key location/Qualifiers

XX FT CDS 145..2070

XX FT /*tag= a

XX PN W09950412-A1.

XX PD 07-OCT-1999.

XX PF 24-MAR-1999; 99WO-JP01512.

XX PR 27-MAR-1998; 98JP-0100467.

XX PA (SAKA) OTSUKA PHARM CO LTD.

XX PA (IKAWA/) IKAWA Y.

XX PI Ikawa Y, Ikawa S, Obinata M;

XX DR WPI: 1999-591318/50.

XX DR P-PSDB: AAK45247.

XX PT New p53 related human gene p51, useful for diagnosis, investigation and

XX PT treatment of cancers and screening for potential cell proliferation

XX PT agents -

XX PS Example 1: Page 154-156; 163pp; Japanese.

XX CC The present sequence represents a human p51 gene, which is related to

XX CC p53 and has cell proliferation regulation and tumour suppression

XX CC activity. The p51 gene can be used in the investigation, diagnosis and

XX CC treatment of diseases such as cancer, with which the p53 family cell

XX CC proliferation regulation is associated. The p51 protein may be used for

XX CC screening potential agonists and antagonists of its regulatory function,

XX CC for use as drugs.

XX CC Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;

Query Match 48.9%; Score 1376; DB 20; Length 2270;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 481 cccaagctccaccttgatgactctctctccatcacccgcacatccctcccaacacagactac 540
Oy 541 ccaagcccgacagcttgcagctgtccctccagcagctcagaccgcagctcgccacc 600
Db 541 ccaagcccgacagcttgcagctgtccctccagcagctcagaccgcagctcgccacc 600
Oy 601 tggacgtattccactgaacttgaagaactctactgtccaaattgcaagaagacatgcccatc 660
Db 601 tggacgtattccactgaacttgaagaactctactgtccaaattgcaagaagacatgcccatc 660
Oy 661 cagatcaaggtgataccccaccctcccaaggagctgtatctcgcccatgtccgtctac 720
Db 661 cagatcaaggtgataccccaccctcccaaggagctgtatctcgcccatgtccgtctac 720
Oy 721 aaaaaagctgaacgactcagcagaggtgtgtgaagcggtgcccacaacatgagctgagccgt 780
Db 721 aaaaaagctgaacgactcagcagaggtgtgtgaagcggtgcccacaacatgagctgagccgt 780
Oy 781 gaattcaacgaggaacagatttgcctcctactgcatcttgatctcgtatgtagagggaacagc 840
Db 781 gaattcaacgaggaacagatttgcctcctactgcatcttgatctcgtatgtagagggaacagc 840
Oy 841 catgcccaagtatgtagaagatcccatcacagaagaacagagtgctgtgtacctaattag 900
Db 841 catgcccaagtatgtagaagatcccatcacagaagaacagagtgctgtgtacctaattag 900
Oy 901 ccaccccggttgagcagtaattcaccagcagctgtgtacaattcatgtgaacgcagct 960
Db 901 ccaccccggttgagcagtaattcaccagcagctgtgtacaattcatgtgaacgcagct 960
Oy 961 tgtgttgaggaatgaacgcctcccaatttaacatgttactcttgaaacagagat 1020
Db 961 tgtgttgaggaatgaacgcctcccaatttaacatgttactcttgaaacagagat 1020


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Db 901 ccaacccggtgtgacgaatcagcagctctgtacaattatgtgtacagcagt 960
Qy 961 tctgttgagagatgaacccgcgcctcaattatcatctgtactctggaacagagat 1020
Db 961 tctgttgagagatgaacccgcgcctcaattatcatctgtactctggaacagagat 1020
Qy 1021 gggcaagccctgggcccgcgcgtctgttaaggcccgcgacatctgtctggccaaagaagac 1080
Db 1021 gggcaagccctgggcccgcgcgtctgttaaggcccgcgacatctgtctggccaaagaagac 1080
Qy 1081 aggaagcgcgatagaatagatcagaagaagcagaatttcggacagatcaaaagacgt 1140
Db 1081 aggaagcgcgatagaatagatcagaagaagcagaatttcggacagatcaaaagacgt 1140
Qy 1141 gatgttaagaagcgcgccttctgttacaagaacacatggtatccaatgacatccatcaag 1200
Db 1141 gatgttaagaagcgcgccttctgttacaagaacacatggtatccaatgacatccatcaag 1200
Qy 1201 aaacgaagatcccccagatgatactgtatacttaccagtgaggggccgtgagacttat 1260
Db 1201 aaacgaagatcccccagatgatactgtatacttaccagtgaggggccgtgagacttat 1260
Qy 1261 gaatgtctgttgaagatacaagaagtccttggaactcatgtacatctctccacagaca 1320
Db 1261 gaatgtctgttgaagatacaagaagtccttggaactcatgtacatctctccacagaca 1320
Qy 1321 attgaaagctacagcagacagcaacagcagcagccagcacttaactctcagaacaa 1376
Db 1321 attgaaagctacagcagcagcaacagcagcagccagcacttaactctcagaacaa 1376
```

RESULT 5

AAZ43913
ID AAZ43913 standard; CDNA: 4846 BP.

AC AAZ43913:

DT 14-MAR-2000 (first entry)

XX Human KET cDNA.

XX KET: anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

KW p53 family; angiogenic; cytotoxic; cancer; human; ss.

XX Homo sapiens.

XX MO9961610-A2.

XX 02-DEC-1999.

XX 25-MAY-1999; 99WO-DE01557.

XX 25-MAY-1998; 98DE-1022985.

XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Paul D, Augustin M, Schmale H, Bamberger C;

XX WPI: 2000-062710/05.

XX P-PSDB: AAY50997.

XX New KET-encoding nucleic acid and related proteins, for diagnosis and

XX treatment of tumors

XX Claim 3; Page 23-26; 28pp; German.

XX This invention describes a novel KET-encoding nucleic acid (I) and its
XX fragments, variants and mutants which has anticancer activity. (I)
XX encodes a protein, (II), involved in control of the cell cycle and
XX apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
XX p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
XX detect (I) in biological samples, specifically angiogenic tumor tissue,

CC including (I) sequences that have a homozygotic deletion and (b) to
CC detect presence or absence of human chromosome 3q27 or murine chromosome
CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor
CC suppressor, particularly in tumors where an alteration in the wild-type
CC p53 allele has not been identified. (I) and (II) may also be used for
CC development of specific cytotoxic agents and for predicting the risk of
CC developing cancer. This sequence represents the human KET cDNA sequence
CC described in the method of the invention.
XX
XX Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;

Query Match 48.4%; Score 1364; DB 21; Length 4846;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy 2 cgtatatacaagaacagtgaagaatgaatttgaacttcaagctgtgccacta 61
Db 1 cgtatatacaagaacagtgaagaatgaatttgaacttcaagctgtgccacta 60
Qy 62 cagctacgcccgcgccttaccatccagcgttctgtagaaa-cccagctcattctctgg 120
Db 61 cagctacgcccgcgccttaccatccagcgttctgtagaaa-cccagctcattctctgg 120
Qy 121 aaagaagttattaccgataccacatgcccagagcacacagacaatgaattcctcagt 180
Db 121 aaagaagttattaccgataccacatgcccagagcacacagacaatgaattcctcagt 180
Qy 181 ccagaggtttccagacatacttggatttcttgaacagcctatatgttcagttacgcc 240
Db 181 ccagaggtttccagacatacttggatttcttgaacagcctatatgttcagttacgcc 240
Qy 241 attgactgaacttggtagatgaaccatagaagaattgtgtgcacaacaaagtttagatt 300
Db 241 attgactgaacttggtagatgaaccatagaagaattgtgtgcacaacaaagtttagatt 300
Qy 301 agcatgactgtatccgcacgtcagagactcgacccgagtgaccccatgtgscacagatc 360
Db 301 agcatgactgtatccgcacgtcagagactcgacccgagtgaccccatgtgscacagatc 360
Qy 361 acgaaccttggggctcctgaacagcatggaacagcagatcagaacggtcctctccac 420
Db 361 acgaaccttggggctcctgaacagcatggaacagcagatcagaacggtcctctccac 420
Qy 421 agtccctataacacagacacagcagcagacagcgtcagcggcctctgcctcagcaag 480
Db 421 agtccctataacacagacacagcagcagacagcgtcagcggcctctgcctcagcaag 480
Qy 481 ccagctccacctctgagtctctctccatcacccgcgcctccctccacaacagactac 540
Db 481 ccagctccacctctgagtctctctccatcacccgcgcctccctccacaacagactac 540
Qy 541 ccaagcccgacagttctgacgtgtcctctccagcagtcgagacccgcaagtctggccac 600
Db 541 ccaagcccgacagttctgacgtgtcctctccagcagtcgagacccgcaagtctggccac 600
Qy 601 tggacgtattccactgaactgaagaactctacttgcgaatgtgcaagaagaccccatc 660
Db 601 tggacgtattccactgaactgaagaactctacttgcgaatgtgcaagaagaccccatc 660
Qy 661 cagatcaaggtatgatacccaactcctcagggagtgattatccgcgcatgtctgtac 720
Db 661 cagatcaaggtatgatacccaactcctcagggagtgattatccgcgcatgtctgtac 720
Qy 721 aaaaagctgagcagctcagcaggtgtgtgaagcgttcccaacatgagctgagcgt 780
Db 721 aaaaagctgagcagctcagcaggtgtgtgaagcgttcccaacatgagctgagcgt 780
Qy 781 gattcaagagagagacagattgcccctctactagtcatttgattcggatgagggagac 840
Db 781 gattcaagagagagacagattgcccctctactagtcatttgattcggatgagggagac 840
Qy 841 catgccagtagtagaagatcccatcacagaagaagagtgctgttacttatgag 900
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|||||
Db 841 catgccagatgtatgaagaatccatccatcagaagaagatgtgtctgtactatgag 900
Oy 901 caaccacagttgtgacgtgaattcaacagacagtcgttacaattcatgttaacagcagt 960
Db 901 |||||||
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Oy 961 tgtgtgtgagagatgaaccgcgcgtcccaatttaaccattgttactctgtgaaccagagat 1020
Db 961 tgtgtgtgagagatgaaccgcgcgtcccaatttaaccattgttactctgtgaaccagagat 1020
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Db 1021 gggcagatccttggcgcgcagcgtctgtttgagcccgagatctgtgtgccaggaagagac 1080
Oy 1081 aggaagcgagatgaagaatagatcatcagaagaagcagaagtttggagaagatcaaaagacgt 1140
Db 1081 aggaagcgagatgaagaatagatcatcagaagaagcagaagtttggagaagatcaaaagacgt 1140
Oy 1141 gatgtacgaagcgcccgcttctgtcagaacacacatgtgtatccagatgacatccatcaag 1200
Db 1141 gatgtacgaagcgcccgcttctgtcagaacacacatgtgtatccagatgacatccatcaag 1200
Oy 1201 aaacgaagaatcccccagatgatgaactgtatatacttaaccagtgaaggcggtgagacttat 1260
Db 1201 aaacgaagaatcccccagatgatgaactgtatatacttaaccagtgaaggcggtgagacttat 1260
Oy 1261 gaaatgctgttgaagaatcaaaagatccctgtgaactcatgacagatccctctcagacaca 1320
Db 1261 gaaatgctgttgaagaatcaaaagatccctgtgaactcatgacagatccctctcagacaca 1320
Oy 1321 attgaacgtacaggaacagacagacagcagcagcagcagcagcagcagcagcagcagcagc 1376
Db 1321 attgaacgtacaggaacagacagacagcagcagcagcagcagcagcagcagcagcagcagc 1376

RESULT 6
AAC66031
ID AAC66031 standard; CDNA: 4849 BP.
AC AAC66031;
XX
XX
XX 21-FEB-2001 (first entry)
DT
XX
XX Human Lung cancer-associated CDNA p63 isoform 5.
DE
XX
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KM vaccine; detection; ss.
XX
XX Homo sapiens.
OS
XX WO200061612-A2.
PN
XX
XX 19-OCT-2000.
PD
XX
XX 03-APR-2000; 2000WO-US08896.
PF
XX
XX 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Wang T, Fan L;
PI
XX MPI: 2000-62839/60.
DR P-PSDB; AAB11361.
XX
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -

XX
PS Claim 25a: Page 240-242; 261pp; English.
CC
XX This invention describes a novel isolated polypeptide (1) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer. In a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. Cda+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
SQ Sequence 4849 BP: 1377 A; 1076 C; 988 G; 1407 T; 1 other;

Query Match 48.4%; Score 1364; DB 21; Length 4849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 2 cgttgatataaagacagttgaaggaatgaatttgaacttcacggtgtgcaccccta 61
Db 1 cgttgatataaagacagttgaaggaatgaatttgaacttcacggtgtgcaccccta 60
Oy 62 cagttactgccccttgaccccttaactcagcgttctgtagaag-cccaagctattctctgg 120
Db 61 cagttactgccccttgaccccttaactcagcgttctgtagaagcccaagctattctctgg 120
Oy 121 aaagaagaatttaacgaatccacacatgcccagagcacacagacaatgaattctcagtt 180
Db 121 aaagaagaatttaacgaatccacacatgcccagagcacacagacaatgaattctcagtt 180
Oy 181 ccaagagtttccagacatcttgagatttcttgaaacagcctatattgtcagtcagccc 240
Db 181 ccaagagtttccagacatcttgagatttcttgaaacagcctatattgtcagtcagccc 240
Oy 241 attgacttgaacttgttgatgaacatcagaagttgttgacaaaagaatttgaagtt 300
Db 241 attgacttgaacttgttgatgaacatcagaagttgttgacaaaagaatttgaagtt 300
Oy 301 agcatgagactgtatcccgatgcagagacgcagacgtgagtgaccccatgtgcccacagtac 360
Db 301 agcatgagactgtatcccgatgcagagacgcagacgtgagtgaccccatgtgcccacagtac 360
Oy 361 acgaacacctggggctctctgaacagcatggaacagagattcagaacggtctctgtccacc 420
Db 361 acgaacacctggggctctctgaacagcatggaacagagattcagaacggtctctgtccacc 420
Oy 421 agtccctataacagacagacgcgcagagacagcgtcagcgccctgccttaacgacag 480
Db 421 agtccctataacagacagacgcgcagagacagcgtcagcgccctgccttaacgacag 480
Oy 481 cccaagctccacctcgaatcctctctcctcatcaaccgcgcacatccctccaacacagactac 540
Db 481 cccaagctccacctcgaatcctctctcctcatcaaccgcgcacatccctccaacacagactac 540
Oy 541 ccaagccgcgacagatttcgaacgtgtccttccagcagcttgagacacgcgaatcggcacc 600
Db 541 ccaagccgcgacagatttcgaacgtgtccttccagcagcttgagacacgcgaatcggcacc 600
Oy 601 tggacgtattccactgaactgaagaactctactctgcaaatgtgaaaagacatgcccatac 660
Db 601 tggacgtattccactgaactgaagaactctactctgcaaatgtgaaaagacatgcccatac 660
Oy 661 cagatcaagtgatgataccccaacctctcagggagctgtttatccgcgcacatgctgtctac 720
Db 661 cagatcaagtgatgataccccaacctctcagggagctgtttatccgcgcacatgctgtctac 720
Oy 721 aaaaaagctgagcagcgtcaaggaagttggtgaagcgtgtcccaacatgagctgagccgt 780
Db 721 aaaaaagctgagcagcgtcaaggaagttggtgaagcgtgtcccaacatgagctgagccgt 780

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OY 761 gaattcaacgaagagacagattgccccctctagctattgattcaggtagagggaacagc 840
DB 761 gaattcaacgaagagacagattgccccctctagctattgattcaggtagagggaacagc 840
OY 841 catgcccagatgtagaagatcccaacaggaagaacagagtgctgttacctatag 900
DB 841 catgcccagatgtagaagatcccaacaggaagaacagagtgctgttacctatag 900
OY 901 ccacccaggtgtgacatgaattcagacagatctgtacaatttcattgttaacagcag 960
DB 901 ccacccaggtgtgacatgaattcagacagatctgtacaatttcattgttaacagcag 960
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DB 961 tctgttgagagatgaacagccgcttccttaattcattgttacctgtgaacccagat 1020
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DB 1021 gggcgaagtcctggcgccgacgctgtctttaggcccggatctgtctgtccaggaagagac 1080
OY 1081 aggaagcgagatgaagatagatcctcagaagcagaagtttcggacagtaacaagaacggt 1140
DB 1081 aggaagcgagatgaagatagatcctcagaagcagaagtttcggacagtaacaagaacggt 1140
OY 1141 gatgtacgaagcgccgcttcctcagacacacatgttatccagatgacatccatcaag 1200
DB 1141 gatgtacgaagcgccgcttcctcagacacacatgttatccagatgacatccatcaag 1200
OY 1201 aaacgaagatcccccagatgatgaactgtatatactacagtgaggcgctgagacttat 1260
DB 1201 aaacgaagatcccccagatgatgaactgtatatactacagtgaggcgctgagacttat 1260
OY 1261 gaaatgctgttgaagaataaagaagtcctctgaactcattgcagctacccctcagaacaca 1320
DB 1261 gaaatgctgttgaagaataaagaagtcctctgaactcattgcagctacccctcagaacaca 1320
OY 1321 attgaacgtacagcacaacagaacagcagcagcagcacttacttcagaanaa 1376
DB 1321 attgaacgtacagcacaacagaacagcagcagcagcacttacttcagaanaa 1376

RESULT 7
AAK58574
ID AAK58574 standard; cDNA; 1347 BP.
XX
XX AAK58574;
AC
XX 16-AUG-1999 (first entry)
DT
XX
XX Human cell regulatory protein p63, isoform hTAp63 gamma, cDNA.
DE
XX
XX Cell regulatory protein; p63; hTAp63 gamma; TAp63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
FH misc_difference 1234
FT /*tag" a
FT /note" "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to maintain
FT the nucleotide numbering given in the
FT specification for this sequence"
PN
XX
XX MO9919357-A2.
XX
XX 22-APR-1999.
XX
XX 02-OCT-1998; 98WO-US21992.
XX

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PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 PA (HARD) HARVARD COLLEGE.
 PI McKeon F, Yang A;
 XX
 XX MPI: 1999-277595/23.
 DR P-PSDB; AAK05955.
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 XX
 PS Claim 1; Fig 11; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are designated as delta1 and TA forms, where the delta1 form lacks the transactivation domain. The present sequence represents a cDNA clone encoding human TAp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta1 isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AA05953-64), polynucleotides (see AAK58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 1347 BP; 374 A; 381 C; 316 G; 275 T; 1 other.

Query Match 47.8%; Score 1346; DB 20; Length 1347;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 145 atgtcccagagacacacagaataatctcccaagtcagaggtttccagatatcgg 204
DB 1 atgtcccagagacacacagaataatctcccaagtcagaggtttccagatatcgg 60
OY 205 gatttctggaaacagccatatgttcagttcagcccatgactgaactttgtgatga 264
DB 61 gatttctggaaacagccatatgttcagttcagcccatgactgaactttgtgatga 120
OY 265 ccatacagaagatgtgtgcacaacaagaattgagattagatgagatcgcagtcag 324
DB 121 ccatacagaagatgtgtgcacaacaagaattgagattagatgagatcgcagtcag 180
OY 325 gactcgtgacatgtgagacccatgtgtgcacacagtaacaacactgtggctctgaacgc 384
DB 181 gactcgtgacatgtgagacccatgtgtgcacacagtaacaacactgtggctctgaacgc 240
OY 385 atgacacagcaatcagaacggctcctcgtccaccagtcctcctaacaacagacacgc 444
DB 241 atgacacagcaatcagaacggctcctcgtccaccagtcctcctaacaacagacacgc 300
OY 445 cagaacacgttcacggcgccctcgtccctacgacagccacagcttcacatgctctc 504

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Db 301 cagaacagcgtcaagcgccctcgccctacgacagcccaagctccacctcgtcgtctc 360
Oy 505 tctccatcaccccgcatccctcccaacacgcgtaccacgcccgcgcgaagtttcagctg 564
Db 361 tctccatcaccccgcatccctcccaacacgcgtaccacgcccgcgcgaagtttcagctg 420
Oy 565 tctccatcaccccgcatccctcccaacacgcgtaccacgcccgcgcgaagtttcagctg 624
Db 421 tctccatcaccccgcatccctcccaacacgcgtaccacgcccgcgcgaagtttcagctg 480
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Oy 1045 ttctgagcccgagatctgtctgtcccaagaagaacagagcggatgaaatagatgacatc 1104
Db 901 ttctgagcccgagatctgtctgtcccaagaagaacagagcggatgaaatagatgacatc 960
Oy 1105 agaaagcagcaagtttcggacagtaacaaagacggtgagtgtacgaagcgccgtttcgt 1164
Db 961 agaaagcagcaagtttcggacagtaacaaagacggtgagtgtacgaagcgccgtttcgt 1020
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Db 1021 cagaacacacagatgatatcagatgacatccatcaagaacacgaagttccccaatgatgaa 1080
Oy 1225 ctgtatacttaacagtgagggcggtgagacttaagaaatgctgttgaaagtaacaaag 1284
Db 1081 ctgtatacttaacagtgagggcggtgagacttaagaaatgctgttgaaagtaacaaag 1140
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Db 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1260
Oy 1405 ctgtgtgagcccgagagagaacatccaaaaacatcgtacgtcttcttagaatcccaag 1464
Db 1261 ctgtgtgagcccgagagagaacatccaaaaacatcgtacgtcttcttagaatcccaag 1320
Oy 1465 ccccaaacagatcagtgtaaccatag 1491
Db 1321 ccccaaacagatcagtgtaaccatag 1347

```

RESULT 8
AAx58573

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ID 10 AAx58573 standard; cDNA: 1551 BP.
XX
AC AAx58573;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cell regulatory protein p63, isoform huTAp63 beta, cDNA.
XX
KW Cell regulatory protein; p63; huTAp63 beta; TAp63 beta; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
OS Homo sapiens.
XX
PN W09919357-A2.
XX
PD 22-APR-1999.
XX
PF 02-OCT-1998; 98WO-US21992.
XX
PR 29-MAY-1998; 98US-0087216.
XX
PR 15-OCT-1997; 97US-0062076.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI McKeon F, Yang A;
XX
DR WPI: 1999-277595/23.
XX
DR P-PSDB; AAY05954.
XX
PT New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
PS Claim 1; Fig 10; 161pp; English.
XX
CC The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta and TA forms, where the delta form lacks the
CC transactivation domain. The present sequence represents a cDNA
CC clone encoding human TAp63 beta. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation, related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAx58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.
XX
SQ Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;

```

Query Match 43.8%; Score 1232; DB 20; Length 1551;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 145 atgtccagagacacagacaatgaattcctcagtcagaggtttccagcatatctcg 204
|||||

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Dh 1 atgtccagagacacagacaatgaattcctcagtcagaggtttccagacatactcg 60
Oy 205 gattcttcggagacagccatattgttcagttcagcccatgtgcttaacttctgtgataa 264
Db 61 gattcttcggagacagccatattgttcagttcagcccatgtgcttaacttctgtgataa 120
Oy 265 ccatcagaagaatgtgtgcagacaacaagaatcagattagacatgagactgtatccgcagtcag 324
Db 121 ccatcagaagaatgtgtgcagacaacaagaatcagattagacatgagactgtatccgcagtcag 180
Oy 325 gactcgcagctgtatgaccccatgtgtgcacagtaacagacgtgggtccctcgaagc 384
Db 181 gactcgcagctgtatgaccccatgtgtgcacagtaacagacgtgggtccctcgaagc 240
Oy 385 atgagaccagcagatccaagaacgctcctcgtccacagtcctcctaacaacagaccagcg 444
Db 241 atgagaccagcagatccaagaacgctcctcgtccacagtcctcctaacaacagaccagcg 300
Oy 445 cagaaacagctcagcgccctcgcctcagcagacagccagctccaccttcgactgtc 504
Db 301 cagaaacagctcagcgccctcgcctcagcagacagccagctccaccttcgactgtc 360
Oy 505 tctccatcaccgcagatccctcacaacacgcagactaacagagccgcagacagttcgagctg 564
Db 361 tctccatcaccgcagatccctcacaacacgcagactaacagagccgcagacagttcgagctg 420
Oy 565 tctctccagcagctgagagacagccagtcgagccagctgtgagctatccacttgaatgaag 624
Db 421 tctctccagcagctgagagacagccagtcgagccagctgtgagctatccacttgaatgaag 480
Oy 625 aaactctactgcacaatgtgcagaagacatgcagccatccagatcaagtgatgcagccact 684
Db 481 aaactctactgcacaatgtgcagaagacatgcagccatccagatcaagtgatgcagccact 540
Oy 685 cctcagagagctgtatccgcgcagctgcctgtctacaaaaagctgcagacgltcagcgag 744
Db 541 cctcagagagctgtatccgcgcagctgcctgtctacaaaaagctgcagacgltcagcgag 600
Oy 745 gtgtgagagcggtgcgccaacatgagctgcagccgtgaattcaagagagagacagttgac 804
Db 601 gtgtgagagcggtgcgccaacatgagctgcagccgtgaattcaagagagagacagttgac 660
Oy 805 cctcctagctatctgtatctgcagtaagagggagacagccatgcagctatgtagaagaatccc 864
Db 661 cctcctagctatctgtatctgcagtaagagggagacagccatgcagctatgtagaagaatccc 720
Oy 865 atcacagagaagacagagtgctgtgtaacctatgagccacccaggttgcagctgaatcc 924
Db 721 atcacagagaagacagagtgctgtgtaacctatgagccacccaggttgcagctgaatcc 780
Oy 925 acgacagctgtgtacaatttcaatgtgttaacagcaattgtgtgagggagatgaaccgctgt 984
Db 781 acgacagctgtgtacaatttcaatgtgttaacagcaattgtgtgagggagatgaaccgctgt 840
Oy 985 ccaatttcaatcatctgttactctctggaacacagagatgagcaagtcctgtgcgcagacgtcg 1044
Db 841 ccaatttcaatcatctgttactctctggaacacagagatgagcaagtcctgtgcgcagacgtcg 900
Oy 1045 tttagagcccgagatcgtgtgtcccgaggaagacagagagcgagatgaagaatgacatc 1104
Db 901 tttagagcccgagatcgtgtgtgtcccgaggaagacagagagcgagatgaagaatgacatc 960
Oy 1105 agaagagcgagagtttggagacgttacaagaacggtgtagtgcaggaagcgccgttttgt 1164
Db 961 agaagagcgagagtttggagacgttacaagaacggtgtagtgcaggaagcgccgttttgt 1020
Oy 1165 cagaacacacatggtatccagatgcacatccatcaagaagaacgagaatcccatgatgaa 1224
Db 1021 cagaacacacatggtatccagatgcacatccatcaagaagaacgagaatcccatgatgaa 1080
Oy 1225 ctgtataacttaacagtgagggcgctgagacttatgaatgctgttgaagaatcaagaag 1284
Db 1081 ctgtataacttaacagtgagggcgctgagacttatgaatgctgttgaagaatcaagaag 1140
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Oy 1285 tccctggagactcatgacgtacacttccctcagcacacaattgaagctacagcgacaagcaa 1344
Db 1141 tccctggagactcatgacgtacacttccctcagcacacaattgaagctacagcgacaagcaa 1200
Oy 1345 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1376
Db 1201 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1232

RESULT 9
AAC66033
ID AAC66033 standard; cDNA; 1551 BP.
XX
XX AAC66033;
XX
XX 21-FEB-2001 (first entry)
DT
XX Human Lung cancer-associated cDNA p63 isoform 7.
DE
XX
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
KM vaccine; detection; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200061612-A2.
PN
XX
XX 19-OCT-2000.
PD
XX
XX 03-APR-2000; 2000MO-US08896.
PF
XX
XX 02-APR-1999; 99US-0285479.
PR 17-DEC-1999; 99US-0466396.
PR 30-DEC-1999; 99US-0476496.
PR 10-JAN-2000; 2000US-0480884.
PR 22-FEB-2000; 2000US-0510376.
XX
XX (CORI-) CORIXA CORP.
PA
XX
XX Wang T, Fan L;
PI
XX
XX WPI; 2000-628399/60.
DR
XX
XX P-PSDB; AAB11363.
DR
XX
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -.
PT
XX
XX Claim 25a; Page 242-243; 261pp; English.
PS
XX
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
XX
XX
XX Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;
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Query Match 43.8%; Score 1232; DB 21; Length 1551;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 145 atgtccagagcagacagacaatgaattcctcagtcagaggtttccagacatactcg 204
Db 1 atgtccagagcagacagacaatgaattcctcagtcagaggtttccagacatactcg 60
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Oy 205 gattctcgaagcagctatatgttcagtcaagccattgacctggaattgtgtgataa 264
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Db 61 gattctcgaagcagctatatgttcagtcaagccattgacctggaattgtgtgataa 120
Oy 265 ccaatcagaagatggtgcgacaacaagaattgagattagcatggaactgtatccgcatgcag 324
    |||||||
Db 121 ccaatcagaagatggtgcgacaacaagaattgagattagcatggaactgtatccgcatgcag 180
Oy 325 gactcggaactgagtgaccacatgtgtgcacagttacagaacctgtgtgtcctcgaacagc 384
    |||||||
Db 181 gactcggaactgagtgaccacatgtgtgcacagttacagaacctgtgtgtcctcgaacagc 240
Oy 385 atggaccagaagattcagaacggtctctcgtccaccagtcctcctataacacagaacagcag 444
    |||||||
Db 241 atggaccagaagattcagaacggtctctcgtccaccagtcctcctataacacagaacagcag 300
Oy 445 cagaagaagtcacagcgccctcgcctcctcagcagacagccagctcgaactcgaatgcctc 504
    |||||||
Db 301 cagaagaagtcacagcgccctcgcctcctcagcagacagccagctcgaactcgaatgcctc 360
Oy 505 tctcacaacccgcacatccctcctcaacacagcagctacacagcccgacagtttcgaacgtg 564
    |||||||
Db 361 tctcacaacccgcacatccctcctcaacacagcagctacacagcccgacagtttcgaacgtg 420
Oy 565 tcccttcagcagtcgagcagcccgcccaagtcgcgacaccttgagcgtatcctcgaactgaag 624
    |||||||
Db 421 tcccttcagcagtcgagcagcccgcccaagtcgcgacaccttgagcgtatcctcgaactgaag 480
Oy 625 aaactctactgcacaaatgcgaagacatgcccatccatcaataagttgtatgacccacct 684
    |||||||
Db 481 aaactctactgcacaaatgcgaagacatgcccatccatcaataagttgtatgacccacct 540
Oy 685 cctcagagggagctgtatctcgcgcacatgctgtctacaaaagctgagacgtcagcagag 744
    |||||||
Db 541 cctcagagggagctgtatctcgcgcacatgctgtctacaaaagctgagacgtcagcagag 600
Oy 745 gtggtggaagcgggtgcgccaacacatgagcgtgagcgtgaaatcaacagagagacattgac 804
    |||||||
Db 601 gtggtggaagcgggtgcgccaacacatgagcgtgagcgtgaaatcaacagagagacattgac 660
Oy 805 cctcctcagtcattgtatgtagtagaggggaacacagcagctacatgtatgataaataccc 864
    |||||||
Db 661 cctcctcagtcattgtatgtagtagaggggaacacagcagctacatgtatgataaataccc 720
Oy 865 atcacaaggaagacagagtgctgtgtacctaatagcaccccgagttgacatgaattc 924
    |||||||
Db 721 atcacaaggaagacagagtgctgtgtacctaatagcaccccgagttgacatgaattc 780
Oy 925 acgacagctctgtacaaattcattgtgtacagcagttgtgtggagggatgaaacccgctg 984
    |||||||
Db 781 acgacagctctgtacaaattcattgtgtacagcagttgtgtggagggatgaaacccgctg 840
Oy 985 ccaatttaataatcatgttactctcgaacacagagatgggcaagtcctctggccgacgctgc 1044
    |||||||
Db 841 ccaatttaataatcatgttactctcgaacacagagatgggcaagtcctctggccgacgctgc 900
Oy 1045 ttgtgggcccggatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1104
    |||||||
Db 901 ttgtgggcccggatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
Oy 1105 agaaagcagcaggttctggacagatcaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1164
    |||||||
Db 961 agaaagcagcaggttctggacagatcaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Oy 1165 cagaacacacatgtaatacagatgcatacacaagaagatcccgagatgatgaa 1224
    |||||||
Db 1021 cagaacacacatgtaatacagatgcatacacaagaagatcccgagatgatgaa 1080
Oy 1225 ctgttatcttaccagtgagggcgccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1284
    |||||||
Db 1081 ctgttatcttaccagtgagggcgccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
Oy 1285 tccctggaactcatgtagtacctctcctcagcacacaattgaaagctacagcgaacagcaa 1344

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Db 1141 tccctggaactcatgtagtacctctcctcagcacacaattgaaagctacagcgaacagcaa 1200
Oy 1345 cagcagcagcaccagcacttactcagaaca 1376
    |||||||
Db 1201 cagcagcagcaccagcacttactcagaaca 1232

RESULT 10
AAx58572
ID AAx58572 standard; cDNA; 1926 BP.
XX
XX AAx58572;
AC
XX
XX 16-AUG-1999 (first entry)
DT
XX
XX Human cell regulatory protein p63, isoform hupAp63 alpha, cDNA.
DE
XX
XX Cell regulatory protein; p63; hupAp63 alpha; Tap63 alpha; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX W09919357-A2.
PN
XX
XX 22-APR-1999.
PD
XX
XX 02-OCT-1998; 98WO-US21992.
PF
XX
XX 29-MAY-1998; 98US-0087216.
PR
XX 15-OCT-1997; 97US-0062076.
XX
XX (HARD ) HARVARD COLLEGE.
PA
XX
XX McKeon F, Yang A;
PI
XX WPI; 1999-277595/23.
DR
XX P-PSDB; AAY05953.
XX
XX New isolated p63 cell regulatory protein for, e.g. treatment of
PT tumours
XX
XX Claim 1; Fig 9; 161pp; English.
XX
XX The present invention concerns the discovery of a new family of
CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
CC which demonstrate certain sequence identity to known tumour
CC suppressor proteins p53 and p73. It has been observed that the
CC intron-exon organisation is conserved between p73 and p53, and from
CC known exon and intron sizes for these 2 genes, it was possible to
CC identify new members of this gene family using a PCR-based strategy
CC of amplifying 2 exons in a conserved domain and their intervening
CC intron. The human p53 gene was localised to chromosomal position
CC 3q27-29. At least 6 different isoforms exist. Splice variants
CC differing at the C-terminus have been designated as alpha, beta and
CC gamma forms, while p63 members differing in the N-terminus are
CC designated as delta1 and TA forms, where the delta1 form lacks the
CC transactivation domain. The present sequence represents a cDNA
CC clone encoding human Tap63 alpha. p63 was detected in a variety of
CC human and mouse tissue. It demonstrates remarkably divergent
CC activities, such as the ability to transactivate p53 reporter genes
CC and induce apoptosis. Cessation or down-regulation of p63 expression
CC may play a critical role in the process of cervical squamous
CC differentiation, both benign and neoplastic. Delta1 isoforms of p63
CC act as dominant negatives towards transactivation by p53 and p63.
CC p63 may also be implicated in haemopoiesis, muscle wasting (e.g.
CC cachexia) and neuronal differentiation and related degenerative
CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
CC AAX58572-83) and anti-p63 antibodies of the invention can be used to
CC identify compounds useful for treating disorders involving such
CC processes, in detection and diagnosis, and in the production of
CC transgenic animals.

```


CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. Mouse p63 cDNA was isolated using
 CC RACE. Sequencing of the amplification product indicated that the
 CC amplified cDNA possessed a truncated N-terminus, i.e. the
 CC transactivation domain was absent. Additional splice variants were
 CC identified by screening a cDNA library with a probe corresponding
 CC to exons 5-9 of p63. At least 6 different isoforms exist. Splice
 CC variants differing at the C-terminus are designated as alpha, beta
 CC and gamma forms, while p63 members differing in the N-terminus are
 CC designated as delta1 and TA forms, where the delta1 form lacks the
 CC transactivation domain. The present sequence represents a cDNA
 CC clone encoding mouse TAp63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta1 isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAX8572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.

XX Sequence 1452 BP; 394 A; 425 C; 341 G; 289 T; 3 other:

Query Match 43.3% Score 1218.2; DB 20; Length 1452;
 Best Local Similarity 90.5% Pred. No. 0;
 Matches 1325; Conservative 0; Mismatches 126; Indels 13; Gaps 2;

QY 29 atgaatttgaacttcacggtgtccaccctacagtagtgcctgcagcccttaactcaag 88
 Db 1 atgaatttgaacttcacggtgtccaccctacagtagtgcctgcagcccttaactcaag 60
 QY 89 cgttctgttagaaa-ccagatcatcttctcttgaaagaagtattatccagccacatg 147
 Db 61 cgttcatagaaaccacagctcatctctcgtggaagaagtattatccagctcagctg 120
 QY 148 tcccgagagacacagacaatgaattctctcagtcacagaggtttccagacatatctggat 207
 Db 121 tccgagagacacacagacaatgaattctctcagtcacagaggtttccagacatatctggat 180
 QY 208 ttctctgaacacagctatatgtctcagtcacagctgaactgaacttggatgaatacca 267
 Db 181 ttctctgaacacagctatatgtctcagtcacagctgaactgaacttggatgaatacca 240
 QY 268 tcagaagaatgtgtcgacaacaagaattgagattagatcagtcagtcacagcagc 327
 Db 241 tcagaagaatgtgtcgacaacaagaattgagattagatcagtcagtcacagcagc 300
 QY 328 tcggagccggaatgacccatgtgtgcacagatgacgaacccctggggtcctcctgaacagctg 387
 Db 301 tcaggacctcagtgaccacatgtgtgcacagatgacgaacccctggggtcctcctgaacagctg 360
 QY 388 gaccagcagatcagaacggtcctcgtccacacagtcctcctaacaacagacacagcag 447
 Db 361 gaccagcagatcagaacggtcctcgtccacacagtcctcctaacaacagacacagcag 420
 QY 448 aacagcgtcagcgcgcctcgtccctacagacagccacagctccacctcagtcctcct 507
 Db 421 aatagcgtcagcgcgcctcgtccctacagacagccacagctccacctcagtcctcct 480
 QY 508 ccaataccgcgcatccctcgaacaacacgactacacagcccgccagcagcttgaagctgcc 567
 Db 481 ccaataccgcgcatccctcgaacaacacgactacacagcccgccagcagcttgaagctgcc 540
 QY 568 ttccagcagtcgacacccgcaagtcggccacctgagcagtttccactgaactgaagaag 627
 Db 541 ttccagcagtcgacacccgcaagtcggccacctgagcagtttccactgaactgaagaag 600

QY 628 ctctactgcgaattgcgaagaagatgcccatccagatcaaggtgatgacccactcct 687
 Db 601 cgttactgcgagattgcgaagaagatgcccatccagatcaaggtgatgacccactcct 660
 QY 688 cagggaagctgtatccgcgcatacctgtctcaaaaaaagctgacacgacgagagtg 747
 Db 661 cagggaagctgtatccgcgcatacctgtctcaaaaaaagctgacacgacgagagtg 720
 QY 748 gtgagacggtgtcccaacacatagctgagccgtgattcaacagagagcagattggccct 807
 Db 721 gtgagacggtgtcccaacacatagctgagccgtgattcaacagagagcagattggccct 780
 QY 808 cctagtcatttgatcgtgtagaggggaacagccatgcccagatgtatgaagatccatc 867
 Db 781 cctagtcatttgatcgtgtagaggggaacagccatgcccagatgtatgaagatccatc 840
 QY 868 acaggaagaacagaggtgtcgtgtagctatgagccacccaggtgtgacatgattcacg 927
 Db 841 acggaagaacagaggtgtcgtgtagctatgagccacccaggtgtgacatgattcacg 900
 QY 928 acagtcgttacaatttcatgtgtacacagcagttgtgtgagggatgaaccgcgtcca 987
 Db 901 acagtcgttacaatttcatgtgtacacagcagtcgtcgtgaggaatgacagacgtcca 960
 QY 988 atttaacattgttactctgtggaacacagatgagcagatcctggcgccgactgctt 1047
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 Db 1021 gagcccgagatcgtgtctgtccaggaagacagagagcggatgtagatgacatcaga 1080
 QY 1108 aagcagcaggttctcgagacatcaaaagacggtgtagtgcagcgcgttccgtcag 1167
 Db 1081 aagcagcaggttctcgagacatcaaaagacggtgtagtgcagcgcgttccgtcag 1128
 QY 1168 aacacacatgttaccagatgacatcacaagaagaatcccaagatgtagactg 1227
 Db 1129 aacacacatgttaccagatgacatcacaagaagaatcccaagatgtagactg 1188
 QY 1228 ttatactacagatgtagggcgtgtgagactatgaatgtgtgtgtagatcaagatgcc 1287
 Db 1189 ctgtacactacagatgtagggcgtgtgagactatgaatgtgtgtgtagatcaagatgcc 1248
 QY 1288 ctggaactcagcagtagtactcctcctcagcaccaattgaacgctacagcgaacagcag 1347
 Db 1249 ctggaactcagcagtagtactcctcctcagcaccaattgaacgctacagcgaacagcag 1308
 QY 1348 cagcagacacagcacttactcagagaacaatctccttcaagcctcctcaggaatgagct 1407
 Db 1309 cagcagacacagcacttactcagagaacaatctccttcaagcctcctcaggaatgagct 1368
 QY 1408 gtggaagcccggaagagaacaatccaaacatctgacgttctctttagacatcccaagcc 1467
 Db 1369 gtggaagcccggaagagaacaatccaaacatctgacgttctctttagacatcccaagcc 1428
 QY 1468 ccaaacgcatcagtgtagccatag 1491
 Db 1429 ccaaacgcatcagtgtagccatag 1452

RESULT 12
 AAX58577
 ID AAX58577 standard; cDNA; 2043 BP.
 XX AAX58577;
 AC AAX58577;
 XX 16-AUG-1999 (first entry)
 DT Human cell regulatory protein p63, isoform deltaNp63 gamma, cDNA.
 XX

KW Cell regulatory protein; p63; hu-deltaNp63 gamma; human;
 KW cancer; tumour suppressor; cell cycle control; apoptosis;
 KW cell proliferation; cell differentiation; therapy; ss.
 XX Homo sapiens.
 OS
 XX MO9919357-A2.
 PN
 XX 22-APR-1999.
 PD
 XX 02-OCT-1998; 98WO-US21992.
 PF
 XX 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX (HARD) HARVARD COLLEGE.
 PA
 PI McKeeon F, Yang A;
 DR MPI: 1999-277595/23.
 DR P-PSDB; MAY05958.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 PS
 XX Claim 1; Fig 14; 161pp; English.
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC identify new members of this gene family using a PCR-based strategy
 CC of amplifying 2 exons in a conserved domain and their intervening
 CC intron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members differing in the N-terminus are
 CC designated as deltaN and TR forms, where the deltaN form lacks the
 CC transactivation domain. The present sequence represents a cDNA
 CC clone encoding human deltaNp63 gamma. p63 was detected in a variety
 CC of human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down-regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. DeltaN isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in haematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see MAY05953-64), polynucleotides (see
 CC AA58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 CC
 XX
 SO Sequence 2043 BP; 536 A; 623 C; 471 G; 413 T; 0 other:

Query Match 41.0%; Score 1154.6; DB 20; Length 2043;
 Best Local Similarity 91.5%; Pred. No. 0;
 Matches 1234; Conservative 0; Mismatches 114; Indels 1; Gaps 1;

Db 121 tcgcagagaccacagacaagcgagttctccagccagaggtctccagcatactggagat 180
 QY 208 ttctcggaaacacccatatagttcagttcagccacttgacttgacttggtgaatacca 267
 Db 181 ttctcggaaacacccatatagttcagttcagccacttgacttgacttggtgaatacca 240
 QY 268 tcagaagatggtgcagcaacaacaagattgagattagatcagatcgtatccgcatgagac 327
 Db 241 tcggaanaatggtgcagcaacaacaagattgagattagatcagatcgtatccgcatgagac 300
 QY 328 tcggaacttgatgaccacacatgtgccaagatagacgaactcgtgggtccctgaagacatg 387
 Db 301 tcagacctcagtcagccacatgtgccaagatagacgaactcgtgggtccctgaagacatg 360
 QY 388 gaccagcagatcagaagcagcgtccctcgtccacacagttccctataacaacagacagcag 447
 Db 361 gaccagcagatcagaagcagcgtccctcgtccacacagttccctataacaacagacagcag 420
 QY 448 aacagcgtcagcgccgcgcgcctcctcagcagacagccagctccaccttgatctctct 507
 Db 421 aatagcgtgacggtccctcgtccctcagcagccagctccaccttgatctctctct 480
 QY 508 ccataccgcgcacccctccacacacagcagccagcagccagcttcgacgtgtcc 567
 Db 481 ccataccgcgcacccctccacacacagcagccagcagccagcttcgacgtgtgtcc 540
 QY 568 ttccagcagtcgagacacgcgcgaagtgcgacacttgacgtatccacttgaaatgaagaa 627
 Db 541 ttccagcagtcgagacacgcgcgaagtgcgacacttgacgtatccacttgaaatgaagaa 600
 QY 628 ctctctgcgaattgcaagaagcagatgcgcacatcagatcaagtgatagccccactct 687
 Db 601 cgtatctgcagatgctgcagacatgccccacatcagatcaagtgatgccccacccca 660
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 Db 721 gtgaagcgtgtccccaacacatgaagctgagcgtgaattcaacagagggagacagttgcct 780
 QY 808 cctaagctatgattcagatgagagggagacacagcagctccagatgataagaatccatc 867
 Db 781 cccaatcattcagatgagagggagacacagcagctccagatgataagaatccatc 840
 QY 868 acaggaagacagagatgtgtgttaccttaagccacccaggttggccactgaattcacg 927
 Db 841 acgggaagcagagatgtgtgttaccttaagccacccaggttggccactgaattcacg 900
 QY 928 acagtcctgtacaattcaatgtgttaacagcagttgtgttggagggatgaaccgcgtcca 987
 Db 901 acagtcctgtacaattcaatgtgttaacagcagctgtgttggagggatgaaccgcgtcca 960
 QY 988 atttaaatcattgttactcttgaaacccaagatgtggcagctctggccagacgtcgttt 1047
 Db 961 atttaaatcattgttactcttgaaacccaagatgtggcagctctggccagacgtcgttt 1020
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 QY 1108 aagcagcaagattcgtgacagtaacaagaacggtgtgattgagaaagcgcgcgtttcgtcca 1167
 Db 1081 aagcagcaagattcgtgacagtaacaagaacggtgtgattgagaaagcgcgcgtttcgtcca 1140
 QY 1168 aacacacatggtatccagatgacatccatcaagaagaacaggaatcccgagatgaacg 1227
 Db 1141 aatacacacaggaatccagatgacatccatcaagaagaacaggaatcccgagatgaacg 1200
 QY 1228 ttatactacagtgaggggcgttgagacttaagaatgtcttgaaagtcaaaagagttcc 1287
 Db 1201 ctgtacctacagtgaggggcgttgagacttaagaatgtcttgaaagtcaaaagagttca 1260

Query Match	36.6%;	Score 1031.2;	DB 20;	Length 2082;
Best Local Similarity	95.7%;	Pred. No. 2e-277;		

Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps. 0;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2001, 21:24:54 ; Search time 108.78 Seconds
(Without alignments)
4900.718 Million cell updates/sec

Title: US-09-670-568B-2
Perfect score: 2816
Sequence: 1 tcgttgatatacaagaacagt.....gcatttggttaaagaana 2816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_MA: *
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2: /cgnl_7/ptodata/1/ina/5B_COMB.seq: *
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4: /cgnl_7/ptodata/1/ina/6B_COMB.seq: *
5: /cgnl_7/ptodata/1/ina/PTUOS_COMB.seq: *
6: /cgnl_7/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.2	8.7	1215	1 US-08-347-792-20	Sequence 20, Appl
2	244.2	8.7	1215	1 US-08-431-357-20	Sequence 20, Appl
3	244.2	8.7	1215	4 US-08-392-542-26	Sequence 26, Appl
4	244.2	8.7	1215	4 US-08-894-327-26	Sequence 26, Appl
5	244.2	8.7	1215	5 PCT-US95-15353-20	Sequence 20, Appl
6	242.6	8.6	1181	2 US-08-486-663A-18	Sequence 18, Appl
7	242.6	8.6	1181	2 US-08-247-904B-11	Sequence 11, Appl
8	242.6	8.6	1181	3 US-08-767-942A-22	Sequence 22, Appl
9	242.6	8.6	1182	2 US-08-184-009-215	Sequence 215, App
10	242.6	8.6	1182	2 US-08-484-956-92	Sequence 92, Appl
11	242.6	8.6	1182	2 US-08-484-956-94	Sequence 94, Appl
12	242.6	8.6	1182	2 US-08-757-653-92	Sequence 92, Appl
13	242.6	8.6	1182	2 US-08-757-653-94	Sequence 94, Appl
14	242.6	8.6	1182	2 US-08-458-356-215	Sequence 215, App
15	242.6	8.6	1182	4 US-08-796-101-46	Sequence 46, Appl
16	242.6	8.6	1303	1 US-08-047-041A-13	Sequence 13, Appl
17	242.6	8.6	1307	1 US-08-047-041A-12	Sequence 12, Appl
18	242.6	8.6	1317	1 US-07-912-011-1	Sequence 1, Appl
19	242.6	8.6	1317	1 US-08-347-792-1	Sequence 1, Appl
20	242.6	8.6	1317	1 US-08-431-357-1	Sequence 1, Appl
21	242.6	8.6	1317	2 US-08-697-221-1	Sequence 1, Appl
22	242.6	8.6	1317	4 US-08-392-542-1	Sequence 1, Appl
23	242.6	8.6	1317	4 US-08-894-327-1	Sequence 1, Appl
24	242.6	8.6	1317	5 PCT-US95-15353-1	Sequence 1, Appl
25	242.6	8.6	1483	4 US-08-796-101-44	Sequence 44, Appl
26	242.6	8.6	1484	2 US-08-184-009-103	Sequence 103, App
27	242.6	8.6	1484	2 US-08-458-356-103	Sequence 103, App

28	242.6	8.6	1511	4 US-08-796-101-168	Sequence 168, App
29	242.6	8.6	1512	2 US-08-184-009-99	Sequence 99, Appl
30	242.6	8.6	1512	2 US-08-458-356-99	Sequence 99, Appl
31	241	8.6	1182	2 US-08-484-956-93	Sequence 93, Appl
32	241	8.6	1182	2 US-08-757-653-93	Sequence 93, Appl
33	238.6	8.5	1355	2 US-08-636-376-1	Sequence 1, Appl
34	234.6	8.3	633	3 US-08-886-280-6	Sequence 6, Appl
35	234.6	8.3	633	3 US-08-870-370-10	Sequence 10, Appl
36	234.2	8.3	1173	2 US-08-184-009-214	Sequence 214, App
37	234.2	8.3	1173	2 US-08-458-356-214	Sequence 214, App
38	234.2	8.3	1173	4 US-08-796-101-45	Sequence 45, Appl
39	228.4	8.1	740	4 US-09-112-437-10	Sequence 10, Appl
40	220.8	7.8	601	2 US-08-484-956-107	Sequence 107, App
41	220.8	7.8	601	2 US-08-484-956-108	Sequence 108, App
42	220.8	7.8	601	2 US-08-757-653-107	Sequence 107, App
43	220.8	7.8	601	2 US-08-757-653-108	Sequence 108, App
44	219.2	7.8	601	2 US-08-484-956-97	Sequence 97, Appl
45	219.2	7.8	601	2 US-08-484-956-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-08-347-792-20
: Sequence 20, Application US/08347792
: Patent No. 5573925
: GENERAL INFORMATION:
: APPLICANT: Halazometis, Thanos D.
: TITLE OF INVENTION: p53 Proteins With Altered
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESS: Howson and Howson
: STREET: Spring House Corporate Cntr., PO Box 457
: CITY: Spring House
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19477
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/347,792
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Bak, Mary E.
: REGISTRATION NUMBER: 31,215
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-540-9206
: TELEFAX: 215-540-5818
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1215 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-347-792-20

Query Match 8.7%, Score 244.2; DB 1; Length 1215;
Best Local Similarity 58.3%; Pred.No. 6.4e-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 506 ctcacatccgcacatccctcacaacacagcagccgcagcaggttcgcagcgt 565
DB 302 CCCTGCTCATCTTCTGTCCTCCCTCCAGAAAACCTACAGGCGAGTACGCTTCCGCTGCG 361

QY 1166 agcacacatgtgtatccagatgatcatcacaagaagaagatccccagatgtgtac 1225
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 Db 956 ACAACAC-----CAGCTCTCTCCACACCAAGAAGAAACACTGTGTGAGAT 1006
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 QY 1226 ttttatctaccagtgagggcgctgagactatgaatgtgttgatcaagaagt 1285
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 Db 1007 ATTTCACCCCTTCAGATCCGGGGCGAGACGCTTCACAAATGTTCGAGAGCTGAATGAGG 1066
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 QY 1286 cccctgagactcatgacagtaactctccacaga 1316
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 Db 1067 CCTTGGAACTCAAGATGCCCAAGCTGGGAA 1097

RESULT 3

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US-08-392-542-26
Sequence 26, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,542
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ. ID NO.: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-392-542-26

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[illegible]

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Db	482	CGCCCCGACCCCGCTCGCGGCATGTGGCATTCACAGCAGTCAACAGACATCAGAGGAGG	541
Qy	746	tgtgtgaagcggtgcccaccacatgaagctgaagcgtgtaattcaagaggaaacagattggcc	805
Db	542	TTGTGAGGCGGTGCCCCACCATGAGCGCTGCTCAATAGCGATG-----GTCTGGGCC	595
Qy	806	ctccctagctatcttgatctcgatgaagagggaacacgcacatgtcccagatgtagaagaatccca	865
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Qy	866	tcaacaggaagaacagagtgctgtctgtatccttatgaagccaccaggttggcactgaattcca	925
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Db	776	CCATCTCTCACCATCATCATCACTGGAAGACTCCAGTGTGTAATCTACTGGGACCGAACACT	835
Qy	1046	tttagagccggagatctgtgtctctgccagaagaacaggaagccggtatgaagaatagacca	1105
Db	836	TTTGAGTGCGCTGTTTGTGTGCTTGCTGTGGAGAGACCCGGCCACAGAGNAGAGAAATCTCC	895
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Qy	1166	agaacacacatgtatctccaatgaatcatccaagaagaagaatgccacagatgtatgac	1225
Db	956	ACAACAC-----CAGCTCCTCTCCCCAGCGCAAAAGAAAGAACCACTGCTGTGGAGAT	1006
Qy	1226	tgttatacttaccagatgaaggcgctgtgagactatataaigtctgttgaagaatcaaaagtt	1285
Db	1007	ATTTCACCCCTTCAGATCCGGGGGCGTAGGAGCGCTTCGAATGTTCCGAGAGCTGATGAGG	1066
Qy	1286	ccctgtgaactcatgctgaactctctcagca	1316
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RESULT

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US-08-894-327-26
Sequence 26. Application US/08894327
Patent No. 6245886
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and peptidomimetics with
TITLE OF INVENTION: structural similarity to human p53
TITLE OF INVENTION: function
FILE REFERENCE: 2973.19998
CURRENT APPLICATION NUMBER: US/08/894,327
CURRENT FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: pctus96/01555
EARLIER FILING DATE: 1996-02-16
EARLIER APPLICATION NUMBER: 08/392,542
EARLIER FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 1215
TYPE: DNA
ORGANISM: Homo sapiens
US-08-894-327-26

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Query Match      8.7%; Score 244.2; DB 4; Length 1215;
Best Local Similarity 58.3%; Pred. No. 6.4e-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

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DB 302 cctctgcatctctgtccctcccaaaaacccacagcgacagtcagttccgtctgtg 361
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DB 362 gctcttgcatcttgtagacgccaactctgtgacttgcagctatccctccgctcaaca 421
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QY 626 aactctactgcgaatctgcaaaacatctgccatccagatcaagtgatgacccaccctc 685
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DB 422 agatgttttgcgaactgcgaagacctgcctgtgcagctgtgtgtatccacacccc 481
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QY 686 ctgagggagctgtatccgcgcacatgcctgtctacaaaaaagctgacagctgaaggag 745
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DB 716 ccaaccatccactacactacatagtgtaaacagcttccgtcgtggtgcagacgaggaagc 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 caatttaactcatgttactctggaacacagagatgaggcaactcctggtgcagcagctgtc 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 776 ccatctctccatcatcacatcagtagaagactccagtgtaattacttggaggaacagct 835
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QY 1046 ttgagggccggtctgtgttctgcccaggaagacaggaagcggtgtgtagatagatcata 1105
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DB 836 tctgagctgtgtctgtgtctgtctgtcctggtgagagacgcgcacagaggaagaatctcc 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1106 gaaagaagaagtttcgagacatcaaaagaacggtgattgtgtaacgcccgtttctgc 1165
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DB 896 gaaagaagaagggagctccacagcgtctcccccagggagcactaagcagacatgcgccca 955
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QY 1166 agaacaacacatggtatccagatgacatcaacaagaacgaagatccccaatgtatgaac 1225
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 956 acaaacac-----cagctcctctcccaagcaagaagaacacatgattgtgagat 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1226 tgttaacttaccagtgagggcgcttgagactatgaatgtgtgtgaagatcaagaagt 1285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1007 attcaaccttacaagacggggcggtgagcgtctcgaatgttctcgaagagcgtcaatgag 1066
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1286 cccctggaactcatgcatcactcctccagca 1316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1067 ccttgaactcaagatgcccagcgttgga 1097
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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SCREEN: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-15353-20

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Query Match      8.7%; Score 244.2; DB 5; Length 1215;
Best Local Similarity 58.3%; Pred. No. 6.4e-59;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 506 ctccatccaccgcatccctcccaacacccgactaccacgagcccgacagtttcgacgtgt 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 302 cctctgcatctctgtccctcccaaaaacccacagcgacagtcagttccgtctgtg 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 566 ccttcagagctgcagacccgacagctgcgcacccctggagctatccactgaactgaaga 625
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 362 gctcttgcatcttgtagacgccaactctgtgacttgcacgtacttccctccgctcaaca 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 626 aactctactgcgaatctgcaaaacatctgccatccagatcaagtgatgacccaccctc 685
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 422 agatgttttgcgaactgcgaagacctgcctgtgcacgtgtggttatccacacccc 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 686 ctgagggagcgtgtatccgcgcacatgcctgtctctaaaaaaaagctgagacgtcaaggag 745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 482 cgcccgacccgcgcgtccgcgcacatgcatctacagcagctacacagcacatgacgag 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 746 tggtagagcggtgcccccaacatgagcgtgagccgtgtaattcaacgagggacagattgcc 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 ttgttagcgcgtgcccccaacatgagcgtgtcagatagcagatg-----gtctgccc 595
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 ctctcagctatttgatcgaagtagaggggaacagccatgcccaglatgtagaagaatccca 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 596 ctctcagcatcttactcagtagaggaatgttgctgtgagagatttgatgacagaa 655
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 tcaaggaagaagcagatgtgtgtgtactctatgagccacccaggttggcactgaatca 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 656 acacttttcgaactgctgtgtgtgtactctatgagccacccgctgaggttgacctgactgta 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 926 cgacagctcttataacttcatgttcaacagcagttgtgtgagggatgataaccgcgcgtc 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 716 CCACATCCACATACATACATGTGTACAGTCTCTGCATGGCGCGCATGAACCGAGGC 775
Qy 986 caatttaatacttctgtctctgtgaacacagagatggcgaagctctgtgacgctct 1045
Db 776 CCATCCTCACCATCATCATCTGCAAGACTCCAGTGTAACTTACTGTGGACGAACTACT 835
Qy 1046 ttgaagcccgatctgtctgtgcccagaagaagacagagcggatgaagatagcatca 1105
Db 836 TTGAGGTGCGGTGTGTGTCTCTCTGCGAGAGACCGCGCACAGAGAAAGAAATCTCC 895
Qy 1106 gaaagcagcaagttctgcagacaglacaaagacggtgagtgatgagagccgcttctc 1165
Db 896 GCAAGAAAGGAGAGCGCTCACCAGAGTCCCGCCAGGAGAGCACTAAGCGAGACTGCCCA 955
Qy 1166 agaacacacatggtatccagatgacatccatcaagaagaagatcccaagatgtaac 1225
Db 956 ACAACAC-----CAGCTCTCTCTCCCAAGCCAAAGAAACCACTGTGATGAGAAAT 1006
Qy 1226 tgtatactaccagtgagggcgctgagactatgaaatctgttgaagatcaaaagat 1285
Db 1007 ATTTCACCTTCAGATCCGCGGCGCTGAGCGCTTGAAATGTTCGAGAGCTGAATGAGG 1066
Qy 1286 ccctggaactcagtcagtagcttccctcagca 1316
Db 1067 CCTTGAACTCAAGAGATGCCCAAGCTGGGAA 1097

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RESULT 6
US-08-486-663A-18
; Sequence 18, Application US/08486663A
; Patent No. 5968761
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume Cottarel
TITLE OF INVENTION: Ubiquitin Conjugating Enzymes
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486.663A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-029CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:

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; NAME/KEY: CDS
; LOCATION: 1..1182
US-08-486-663A-18

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Query Match      8.6%; Score 242.6; DB 2; Length 1181;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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Qy 506 ctcatcaccgcgcattccctccaaacaccgactaccagcgcgcagatgttgcagtg 565
Db 275 CCCTGTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 334
Qy 566 ccttcagcagtcgagcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 625
Db 335 GCTTCTTGTGATTTGTGGACAGCCAAAGTGTGTGACTTGTGACGCTTGTGCTCTCA 394
Qy 626 aactctactgcgaattgcgaagacatgcccatcagaatcagaagtgatgaacccactc 685
Db 395 AGATGTTTTGCCAATCGGCAAGACCTGCGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 454
Qy 686 ctcaaggagctgttataccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 745
Db 455 CGCCCGGACCCGCGCTCCGCGCATGCGCATGTCTACAGCAGTACAGCAGTACAGCAG 514
Qy 746 tggtagacggtgtgcccacacatgagctgagcgcgtgaattcaacgaggaacagatt 805
Db 515 TTGTAGGCGCTGCCCCCAACCATGAGCCCTGCTCAGATAGCATG-----GTCGTGGCC 568
Qy 806 ctctcagtcatttgatctcagtagaggggaacacgcatgcccagatgtagaagatccca 865
Db 569 CTCCTCAGACTTATTCGAGATGGAAGAAATTCGATGAGATTTGGATGACAGAA 628
Qy 866 tcaagaagaacagagtgctgtgtacattatgagccacccaggttgcagctgaattca 925
Db 629 ACACCTTTTCGACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 688
Qy 926 gacacgcttgtagcaattcattgtagaagcagtgtagtgtagtgtagtgtagtgtag 985
Db 689 CCACATCCACTACACTACATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 748
Qy 986 caatttaatacttctgtctctgtgaacacagagatggcgaagctctgtgacgctgt 1045
Db 749 CCATCCTCACCATCATCATCTGCAAGACTCCAGTGTAACTTACTGTGGAGCGAACACT 808
Qy 1046 ttgaagcccgatctgtgtctgtgcccagaagaagacagagcggatgaagatagcatca 1105
Db 809 TTGAGGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 868
Qy 1106 gaaagcagcaagttctgcagacaglacaaagacggtgagtgatgtagaagcccgctt 1165
Db 869 GCAAGAAAGGAGAGCGCTCACCAGAGTCCCGCCAGGAGGACTAAGGAGAGTGTGCCCA 928
Qy 1166 agaacacacatggtatccagatgacatccatcaagaagaagatcccaagatgtaac 1225
Db 929 ACAACAC-----CAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 979
Qy 1226 tgtatactaccagtgagggcgctgagactatgaaatctgttgaagatcaaaagat 1285
Db 980 ATTTCACCTTCAGATCCGCGGCGCTGAGCGCTTGAGATGTTCGAGAGCTGAATGAGG 1039
Qy 1286 ccctggaactcagtcagtagcttccctcagca 1316
Db 1040 CCTTGAACTCAAGAGATGCCCAAGCTGGGAA 1070

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RESULT 7
US-08-247-904B-11
; Sequence 11 Application US/08247904B
; Patent No. 5981699
GENERAL INFORMATION:
APPLICANT: Rolfe, Mark
APPLICANT: Eckstein, Jens W.

```

Query Match	8.6%;	Score 242.6;	DB 2;	Length 1181;
Best Local Similarity	58.2%;	Pred. NO. 1.8e-56;		
Matches 472;	Conservative	0;	Mismatches 324;	Indels 15; Gaps 2

Y	506	ctccacacacccgcacatccccccacacacccgactaccagcgcccgcaagatttcgagtg	56
D	275	CCCTGCACTCTTCGTCTCCCTTCCACAGAAAACCTACAGGAGCGTACAGGTTTCGCTGG	33
Y	566	ccctccagcagtcgagacacgcgaagtcgagccactgtagcattcacctgcaactgaaga	62
D	335	GGTTCTTGCATTTGGGAGAGCCAACTCTGTACTTGGACGTACTCTCCCGCCCTCAACA	39
Y	626	aacttactgccaattgtgcaagaacatgtcccatccagatlaagatgtatgacccaccc	68
D	395	AGATTTTTCGCAACCTGGCCACAGACCTGCCGTCGTCAGCTGTGGTTGATTCCACACCC	45
Y	686	ctcagagagactgttatccgcgcacatgcctgtctcaaaaaagctgagcaagctcaagag	74
D	455	CGCCCGGACCCGCGTCCGCCCATTCGACCAATTCACAAAGCTACACGACATGACGAGG	51
Y	746	tgtgtgaagcgtgtgcccaacacatgacgtcgagccgtgatatccacagcggaacagattgcc	80
D	515	TTTGTGAGGCGCTCCGCCACCATGAGCGCTCTCAAGTACCGTGC-----GTCGGGCC	56
Y	806	ctctcagtcacttgattcgagtagagagggaaacagccatgtgccagatgtlagaagaatcca	85
D	569	CTCTCTACGACTCTTATCCAGTAGGAGAAATTTGCGTGGAGATATTGGATGACAGAA	62
Y	866	tcaacaggaagacagatgtgtcgtgttaccttatagaccaccccaagttgtgcactgaatca	92
D	629	ACACTTTTGCACATAGTGTGGTGGCTCCCTATATAGCCGCGCTAGGTTGGCTCTACATGA	68
Y	926	cgcacagctctgtacaattcatgtgtacaacagcagttgtgtgagggatgaacgcgcgtc	98

Db 689 CCACCACTCCACTCAACAATCAATGTTGAACAGTTCTTCGCATGGCGGCATGAACCGGAGC 748

QY 986 caattttaaactatglttactctcgaacaacccagagatgggcaagtcctcggccgaagctgtc 104

Db 749 CCATCTCCCTCACTCATCAACACTGGAAAGACTCCAGTGGTAAATCTACTGGGACGGMAACGCT 111

QY 1046 ttgaagcccgagctctgctgtcttgcgccgaagaagaacaggaagcgagatgaagatgactca 1107

Db 809 ttgagctggctgtttttgtgtccctgcctcgtggagagacggccacagagaaagacaatcttc 868

QY 1106 gaagacagcaagatttcgcgaagacagcaagaagcgtgtgactgaagcgcccgcttgc 1167

Db 869 GCAGAGAAAGGGAGAGCTTACCACAGCGTGGCCCCCAGAGAGACTAAGCAGACACTGGCCA 928

QY 1166 agaacacacatglatccagatgatacctcaagaagaagaagatctcccaagttgtaac 1225

Db 929 ACAACAC-----CAGCTCCCTCTCCACAGCAAAAGAAACCACTCGATGGAGCAAT 979

QY 1226 tgtatacttaaccggtgaagggccggtgaagactatgaatgtcgtctggaagatcaaaagat 1285

Db 980 ATTTCACCCCTTCAGATCCGtggggcgtgagagcgctgcgaatgtttccgaagactgaatgagg 1039

QY 1286 ccctgaagactatgcagttactctccacga 1316

Db 1040 CCTTGGAACCTAAGATGCCCAAGGCTGGGAA 1070

RESULT 8
US-08-767-942A-22

Sequence 22, Application US/08767942A
Patent No. 6068982

GENERAL INFORMATION:

APPLICANT: KOLIE, Ch...

APPLICANT: Bert...

APPLICANT: Damagm

APPLICANT: Draett

APPLICANT: Guilla

NUMBER OF INVENTIONS

NUMBER OF SEQUENCE
CORRESPONDENCE ADD

ADDRESSEE: FOLIE

STREET: One Pos

CITY: Boston

STATE: MA
COUNTRY:COUNTRY: USA
ZTD: 00100 0170

TEL: 02109-2110
COMPUTER READABLE

MEDIUM TYPE: F10

COMPUTER: IBM PC

OPERATING SYSTEM

SOFTWARE: Patent

CURRENT APPLICATION NUMBER

FILING DATE: 17-

ATTORNEY/AGENT INFO

NAME: Vincent, M

REGISTRATION NUMER

REFERENCE/DOCKET

TELECOMMUNICATIONS
TELEPHONE: 617-861-1111

TELEPHONE: 017-8
TELEFAX: 617-832

INFORMATION FOR SEQ 1

SEQUENCE CHARACTERI

LENGTH: 1181 bas

TYPE: nucleic ac

CINCINNATI: DO
 TOPOLOGY: 7400x

MOLECULE TYPE: CDN

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1179

9-06-101-942A-22

QY 1046 ttgaagcccgagatctgtgtctgtcccaagaagaacagagcgatgaatgacatca 1105
Db 809 TTGAAGTCCGCTGTTGCTGTCTGTCTGGAGAGACCGCCACAGAGAGAGATCTCC 868
QY 1106 gaaagcagcaagttctggacagctacaagaacggtgtgtgtgagaaagccgcttgc 1165
Db 869 GCAAGAAAGGGAGCCCTCACCAGAGCTGCCCCAGGAGACCTAACGACGACTGCCCA 928
QY 1166 agaacacacatggtatccatgacatccatcaagaagaatcccaagatgagac 1225
Db 929 ACAACAC-----CAGCTCTCTCTCCACAGCCAAAGAAACCACTGATGAGAAAT 979
QY 1226 tgtatactacagtgagggccgtgagacttaagaatgctgtgtgaatgaagat 1285
Db 980 ATTTCACCCCTTCAATCCGTGGGGGTGACGCGCTTCGAGATGTTCCAGAGCTGAATGAG 1039
QY 1286 ccttggaactcagtcagctaccccttcagca 1316
Db 1040 CCTTGAACCTCAAGGATGCCAGGCTGGAA 1070

RESULT 10

US-08-484-956-92
; Sequence 92, Application US/08484956
; Patent No. 5843634

GENERAL INFORMATION:

APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA

TITLE OF INVENTION: DETECTION OF p53 MUTATIONS
NUMBER OF SEQUENCES: 114

CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSHOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956

FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601

FILING DATE: 09-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164

FILING DATE: 09-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359

FILING DATE: 06-JUN-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384

FILING DATE: 04-JUN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330

FILING DATE: 07-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: CARROLL J, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: F0RS-01801

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 92:

SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-92

Query Match 8.6%; Score 242.6; DB 2; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 506 ctccacacacgagcgcacccctcccaacacagctacccagccgacagttctgacggt 565
Db 275 CCTGTGATCTTCTGTGCTGCTCCAGAAACCTACAGAGGACGCTTCCGCTG 334
QY 566 ccttcagcagtcgagcagccgcaagtcggccacgtgacglatccactgaactgaaga 625
Db 335 GCTTCTTGTGATCTTGTGGAGAGCCAGCTGTGACTTGCACGCTACCTCCCTCCACAA 394
QY 626 aactctactgccaatgtgaagacatgcccacatccagatcaagtgatgacccactc 685
Db 395 AGATGTTTGGCCAACTGGCCAAAGACCTGCTGTGACCTGTGATGATTCACACCTCC 454
QY 686 ctcaaggagcgtgtatccgcgcacatgctgtctacaacaaacgtgagcgtcaagag 745
Db 455 GCGCCGCGACCGCGCTGCGCCCATGCGCATCTCAAGCACTCAACAGACATGACGAGG 514
QY 746 tggtagacggctgccccacatgagctgagcctgtaattcaagagggacagatgccc 805
Db 515 TTGTGAGGCGCTGCCCCACCATATGAGCGCTCTCAGATAGGATG-----GTCTGCCCC 568
QY 806 ctccatgacttgaatctgagtagaaggaaacagccatgcccagatgtagaagatccca 865
Db 569 CTCCACAGCATCTTATCCGAGTGGAGAGAAATTTGCGTGTGAGATATTGATGACAGAA 628
QY 866 tcaagaggaagcaagtgctgtgtacattagaccacccagttggaactgaattca 925
Db 629 ACACCTTTTCGACATGATGTGTGTGCTGCTGATGAGCCGCTGAGCTGTGACATGTA 688
QY 926 cgacagctctgtacaattcatgtaacagcagtggtgtgtgagaggaagaaacgcgcgt 985
Db 689 CCACATCCTACATACATACATATGTAACAGTTCTCTCATGCGCGGATATACCGGAGGC 748
QY 986 caatttaactatgttactctggaacagagatgaggcaagtcctggtgcgcagctgtc 1045
Db 749 CCATCTCACCACATCATCACTGGAAGACTCCAGTGTGTAATCTACTGCGAGGAGACGCT 808
QY 1046 ttgaagcccgagatctgtctgtgcccagaagagacagagcggtgtgagataagatca 1105
Db 809 TTGAAGTCCGCTGTTGCTGTCTGTCTGGAGAGACCGCCACAGAGAGAGAAATCTCC 868
QY 1106 gaaagcagcaagttctggacagctacaagaacggtgtgtgtgagaaagccgcttgc 1165
Db 869 GCAAGAAAGGGAGCCCTCACCAGAGCTGCCCCAGGAGACCTAAGCGAGACTGCCCA 928
QY 1166 agaacacacatggtatccatgacatccatcaagaagaagatcccaagatgagac 1225
Db 929 ACAACAC-----CAGCTCTCTCTCCACAGCCAAAGAAACCACTGATGAGAAAT 979
QY 1226 tgtatactacagtgagggccgtgagacttaagaatgctgtgtgaatgaagat 1285
Db 980 ATTTCACCCCTTCAATCCGTGGGGGTGACGCGCTTCGAGATGTTCCAGAGCTGAATGAG 1039
QY 1286 ccttggaactcagtcagctaccccttcagca 1316
Db 1040 CCTTGAACCTCAAGGATGCCAGGCTGGAA 1070

RESULT 11
US-08-484-956-94
; Sequence 94, Application US/08484956

PatentNO. 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYANICHEV, VICTOR I.
APPLICANT: BROM, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF P53 MUTATIONS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARPOLL J, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-94

	Query Match	8.6%	Score 242.6	DB 2	Length 1182
	Best Local Similarity	5.2%	Pred. No. 1.8e-58		
	Matches 472	Conservative	0	Mismatches 324	Indels 15
				Gaps	2
QY	ctccacacaccgcacatccctcccaacacacgataccagccgcagattcgcagctgt	565			
DB	275 cccgtctatcttctgtcccttcccgagaaacctaccaggcagctatgctgtcg	334			
QY	566 ccttcacagcagtcgacacccgcaagtcgycacactggaacttaccatgaactgaaga	625			
DB	335 gctttcttcattcttgaggacagccaaagtctgtaattgcacgtactccctccacaa	394			
QY	636 aactctaactgcaaatattgaaagaactgcccacatccagatcaagtgtatgaccccaacc	685			
DB	395 agattttttggccacattggccagaccctggccctgtgacgttgagggttatggtccacacccc	454			

OY	686	ctcaggagagctgttatctccgagccatctcgctctacaaaaagctgaagacgtccagggag	745
Db	455	CGCCCCGACCCCGCGTCCGGCCATGGCCATCTACAGCAGCTCACAGCATGAGGAGG	514
OY	746	tgtgtgaagcggltgcccacaacagaaagctgaagccgtgaattcacaagaggaattgccc	805
Db	515	TTTGAGAGCGGTGCCCCACCATGAGCGCGTGGCTGACATATGCGATG-----GTCTGGCCC	568
OY	806	ctctcagtcatttgattctcgagtagaagggaacacgcatgcccagtatctagaagaatccca	865
Db	569	CTCTCGACGACTTTATTCGAGTGGAAAGAAATTTGGTGTGGATTTGGATGACACAA	628
OY	866	tcacagaagaacagagatgtctgtgtaacctatgaagccaccocagctgcagctgaatca	925
Db	629	ACACTTTTTCGACATAGTGTGTGTGTGCCCTATGAGCGCGCTGAGTTGGCTGTGACTGTA	688
OY	926	cgacagctctgttacaatttcatgtgtcaacagcagttgtgttggaagatgaacgcgcgtc	985
Db	689	CCACCATCCACTACAACTACATGATGTGTAAAGATGTTCTCGATGGCGCGCATGAACCGGAGAC	748
OY	986	caattttaatcatattgttaccctctgaaacacagatgaggaaagtcctctggccgaagctgtc	1045
Db	749	CCATCTCTACCATATCATACACTGGAAGACTCCAGTGTGTAATTACTGGGACGAAACACT	808
OY	1046	ctgaagcccgagatctgtctgtctgcggaagaaacagaaagccgagatgaagatgaatca	1105
Db	809	TTGAGGTGGCGTGTGTGGCTGTGTCGTGGGAGAACCGCGGCGCACAGAGGAAGAAATCTCC	868
OY	1106	gaaagcagcaagttctcgacacagtaacaaagacggtgtatgtgtcgaagcgcgccgttgc	1165
Db	869	GCAAGAAAGGGGAGCCTCACACAGACACTGCCCCCAGGAGGACACTAAAGAGAGCACTGGCCA	928
OY	1166	agaacacacactlgtatctcaga tgaacatcacaacaaagaaacgaagatctcccaagatgaac	1225
Db	929	ACAAACAC-----CAGTCTCTTCTCCCAAGCCAAAGAAAGAAACACTGATGGAGAT	979
OY	1226	tgttatacttaacagatgaagggccgttgagaactatgaatgtctgttgaaatcaaaagat	1285
Db	980	ATTTCACCCCTTCAGATCCGTGGGCGTGAAGCGCTTCGAGATGTTCCGAGAGCTGATGAGG	1039
OY	1286	ccctggaactcatgtcagtlactctccacaga	1316
Db	1040	CTTTGGAACCTCAAGATGCCCAAGCTGGGAA	1070

RESULT 12
US-08-757-653-92
Sequence 92, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SPOUNCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:


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Db      569 CTCCACACATCTTATCCGAGCTGGAAGAAATTGCGTGTGAGATTTGGATGACAGAA 628
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Db      629 ACACCTTTCGACATGATGTGGTGGCCCTATGAGCCCGCTGAGTGTGGCTCTGACTGTA 688
Qy      926 cgacagctctgtacaattcattgtgtacacagagtgctgtgtgaagagatgaacccgctc 985
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Qy      986 caatttaacatctgttactcttgaagaaacagagatgaggaagctcctggcgacgtctgt 1045
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Qy      1106 gaaagcagcaagtttcgagacagtaacaagaagcgtgtgtatgaggaagcccggttctgc 1165
Db      869 GCAAGAAAGGGAGGAGCTTCACACAGAGCTGCCCCAGGAGACTAAGGAGCAGCAGCTGCCA 928
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Db      929 ACAACAC-----CAGCTCTCTCCCAAGCCCAAGAAACCACTGATGAGAAAT 979
Qy      1226 tgtatacttaccagtgagggcggtgagacttataaagtctgttgaagatcaagaagt 1285
Db      980 ATTTCACCTTCAGATCCGTGGGCGCTGAGCGCTTCGAGATGTTCGAGAGCTGAATGAGG 1039
Qy      1286 cccctgaactcatgtaagtaacttccctcagca 1316
Db      1040 CTTTGAACCTCAAGATGCCCAAGCTGGGAA 1070

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RESULT 14

US-08-458-356-215

Sequence 215, Application US/08458356

Patent No. 5942235

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Tartaglia, James

APPLICANT: Cox, William I.

TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY

NUMBER OF SEQUENCES: 217

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/458,356

FILING DATE: 02-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184,009

FILING DATE: 19-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2530

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

TELEX: 425066CURTMS

```

; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-458-356-215

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Query Match      8.6%, Score 242.6; DB-2; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1,86-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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Qy      566 cctccagcagtcgagacccgacagtcgcccacttgacgtatccactgaactgaaga 625
Db      335 GCTTCTTCATTTCTGGAGCAGCCAGCAAGTCTGTGACTTGCACGTACTCCCTGCCCTCAACA 394
Qy      626 aactctactgcgaattgcaaaagacatgcccatccacatcaaggtga tgaaccacatc 685
Db      395 AGATGTTTGGCAACTGGGCAAGACCTGCCCTGTGACACTGTGGGTGATTCACACACCC 454
Qy      686 ctcaaggagctgttataccgagccatgctctctcaaaaaagctgagcagctcaagag 745
Db      455 CGCCCGGACCGCGCTCGCGGCATGCGCATCTACAAACAGTCAAGACATGAGGAGG 514
Qy      746 tggtagaagcgtgtgcccaacatgagctgagcgtgaaattcaagaggaagacagattgcc 805
Db      515 TTGTAGAGGCGCTGCCCCACCATGAGCCCTGCTCAGATAGCATG-----CTGTGGCC 568
Qy      806 ctccatgaatcttgaatctgagtagaagggaagacagccatgcccagatgtagaagaatccca 865
Db      569 CTCCACACATCTTATCCGAGTGAAGAAATTGCGTGTGAGATTTGGATGACAGAA 628
Qy      866 tcaagaggaagacagagtgctgtgtacttataagcccccaggttgacactgaatca 925
Db      629 ACACCTTTCGACATGATGTGGTGGCTGAGACCCCTGAGGTGGCTGTGACTGTA 688
Qy      926 cgacagctctgtacaattcattgtgtacacagagtgctgtgtgaagagatgaacccgctc 985
Db      689 CCACCATTCACATACATACATGTGTAACTGTTCTGATGGCGGCGCATGAACCGGAGGC 748
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Db      749 CCATCCTCACCATCATCATCATGGAAGACCTCAAGTGAATCTACTGGAGCGAACACT 808
Qy      1046 ttgagcccgagatctgtgtcttgcaggaagaagacaggaagcgagatgaatagatca 1105
Db      809 TTGAGGTGCGTGTGTGCTGCTGCTGGAGAGACCGCGCACAGAGAGAGAAATCTCC 868
Qy      1106 gaaagcagcaagtttcgagacagtaacaagaagcgtgtgtatgaggaagcccggttctgc 1165
Db      869 GCAAGAAAGGGAGGAGCTTCACACAGAGCTGCCCCAGGAGACTAAGGAGCAGCAGCTGCCA 928
Qy      1166 agaacacacatgtaacagatgacatccatcaagaagaagatccacagatgtagaac 1225
Db      929 ACAACAC-----CAGCTCTCTCCCAAGCCCAAGAAACCACTGATGAGAAAT 979
Qy      1226 tgtatacttaccagtgagggcggtgagacttataaagtctgttgaagatcaagaagt 1285
Db      980 ATTTCACCTTCAGATCCGTGGGCGTGAAGCGTTTCCGAGATGTTCGAGAGCTGAATGAGG 1039
Qy      1286 cccctgaactcatgtaagtaacttccctcagca 1316
Db      1040 CTTTGAACCTCAAGATGCCCAAGCTGGGAA 1070

```

RESULT 15

US-08-796-101-46

Sequence 46, Application US/08796101
Patent No. 6183752
GENERAL INFORMATION:
APPLICANT: EPSTEIN, STEPHEN E.
APPLICANT: FINKEL, TOREN
APPLICANT: SPEIR, EDITH
APPLICANT: ZHOU, YI FU
APPLICANT: ZHU, JIANHUI
APPLICANT: BRIDLE, LORNE
APPLICANT: PINCUS, STEVEN
TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESS: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 05-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 764-5574
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-796-101-46

Query Match 8.6%; Score 242.6; DB 4; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.8e-58;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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DB 275 CCCGTCATCTTGTGCTCCCTCCAGAAACCTACCAAGGCGAGCTACGGTTCCGCTGG 334
QY 566 cctccagcagctcgagacccgcaagtcgagccacctcgacgtatccactgaactgaaga 625
DB 335 GCTTCTTGCAATTCGGAGCAGCAAGTCGTGACTGACGTACTGCCCTGCCCTCAACA 394
QY 626 aactctactgcgaatcgacaagacatgcccacatccagatcaagtgatgatacccccac 685
DB 395 AGATGTTTGGCCAACTGGCCAAAGACCTGCTGCTGCACTGTGGTTGATTCACACCCC 454
QY 686 ctccagagagctgtatccgagccatgctgtctacaacaaagctgagcaagctgacgagag 745
DB 455 CGCCCGGACACCGGCTCGCGCCATGSCCATGTACAAAGCAGTCACAGCAACATGACGAGG 514
QY 746 tggtagaagcggtgcccacacatgagctgagcggtgaattcaagagaggaacagattggcc 805
DB 515 TTGAGAGCGCTGCGCCACACATGACGCTGCTCAGATAGCGATG-----GTCGCGCC 568
QY 806 ctccatgacttggatccgtagtagagaggaacagccatgcccagtagtagaagatccca 865
DB 569 CTCCTCAGCACTTATCCGAGTGAAGAAATTGGCTGTGAGATTTTGGATGACAGAA 628

QY 866 tccaggaagacagagtgctgtgcttaacttaagccaccgccaggttgcaactgaattca 925
DB 629 ACACTTTTCACATATGATGCTGTGCTGCTTATGACCGCTGAGGTGGCTCTGACTGTA 688
QY 926 cgaagctctgtacaattcattgtaacagcaggtgtgttgaggagatgaacgcgcgtc 985
DB 689 CCACATCCCACTACACTACATGATGTAACAGTCTTCGATGGCGGCGCATGAAACCGGAGGC 748
QY 986 caatttaacatgttactctgtgaacacagagatggggaagtcctgggcccagctgtct 1045
DB 749 CCATCTTCACCATCATCATCTGACCTGGAAGACTCCAGTGTATTTACTGGGACGACAGCT 808
QY 1046 ttgagcccgatcgtgtcttgccaggaagacaggaagcgga tgaagatagcatca 1105
DB 809 TTGAGTGCGGTGTTGTGCTGCTGCTGAGAGACCGGCGCACAGAGAAATCTCC 868
QY 1106 gaaagcagcaagtttcgagcagtaacaagaacggtgtagtgcgaagcgccggttcgtc 1165
DB 869 GCAAGAAAGGAGACCTCACACGAGAGCTGCCCCAGGAGACACTAAGCGACACTGCCCA 928
QY 1166 agaacacacatggtatccagatgacatccatcaagaagaagatcccgatgagaaac 1225
DB 929 ACAACAC-----CAGCTCTCTCCCAAGCCAAAGAAAGAACCTGTGATGAGAAAT 979
QY 1226 tgtatactaccagtgagggccgtgagactatgaactgctgttgaaagatcaaaagat 1285
DB 980 ATTTCACCTTCATCATTCGGTGGGCGGTGAGGCGCTTGAGATGTTCCGAGACTGAAATGAGG 1039
QY 1286 ccctggaactatgacgtacatccttcctgaagca 1316
DB 1040 CTTGGAACCTCAAGATGCCCAAGCTGGGAA 1070

Search completed: August 8, 2001, 00:15:37
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
9814.954 Million cell updates/sec

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Perfect score: 2816
Sequence: 1 tcgttgatacaagaacagt.....gcacttggttaaagaaa 2816

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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223: gb_est143:*
224: gb_est144:*
225: gb_est145:*
226: gb_est146:*
227: gb_est147:*
228: gb_est148:*
229: gb_est149:*
230: gb_est150:*
231: gb_est151:*
232: gb_est152:*
233: gb_est153:*
234: gb_est154:*
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247: gb_est167:*
248: gb_est168:*
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250: gb_est170:*
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252: gb_est172:*
253: gb_est173:*
254: gb_est174:*
255: gb_est175:*
256: gb_est176:*
257: gb_est177:*
258: gb_est178:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


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RESULT 2
LOCUS AM368384 582 bp mRNA EST 04-FEB-2000
DEFINITION PM2-HT0190-081099-001-e08 HT0190 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM368384
VERSION AM368384.1 GI:6873034
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-HT0190-
081099-001-e08&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 582.
Location/Qualifiers
1. 582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="HT0190"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 180 a 130 c 149 g 123 t
ORIGIN
Query Match 19.2%; Score 541.2; DB 115; Length 582;
Best Local Similarity 98.2%; Pred. No. 3.4e-134;
Matches 558; Conservative 0; Mismatches 8; Indels 2; Gaps 1;

811 agtcattgattcagatagagggaacagccatgccagtagtgaagatcccatca 870
|||||
3 agtcattgattcagatagagggaacagccatgccatgtagaatacccatcaca 62
|||||
871 ggaagacagagatgctggttacctatagagcca--cccaggttgcaatgaatcaga 928
|||||
63 ggaagacagagatgctggttacctatagagccaacccaggttgcaatgaatcaga 122
|||||
929 cagctcttgcaatcattcatatgtaacagcagttgtgttgagagatgaacccgctcca 988
|||||
123 cagctcttgcaatcattcatatgtaacagcagttgtgttgagagatgaacccgctcca 182
|||||
989 tttaatcatgttactctcgtgaacacagatggcgaagtccttggtccgagctcttg 1048
|||||
163 ttttattcatttttttactctcgtgaacacagatggcgaagtccttggtccgagctcttg 242
|||||
1049 aggcccgagatctgtctgtcccaagagagacaggaagcgagatgaatcacaagaa 1108
|||||
243 aggcccgagatctgtctgtcccaagagagacaggaagcgagatgaatcacaagaa 302
|||||
1109 agcaagcagtttcgcgacgatacaagaacggtgatagttaagaagcccgcttcgta 1168
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Db 303 AGCAGCAAGTTTCGACAGTACAAAGACGATGATGACGAAGCCCGCTTTCGCACA 362
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Qy 1169 acacacatggtatccacagatgacatccatcaagaagaagatcccaagatgatagt 1228
|||||
Db 363 ACACACATGATGATCCAGATGACATCCATCAGAAAGCAAGATCCCATGATGAACTGT 422
|||||
Qy 1229 ttacttaccagtgagggcgctgagactatgtaatctgtctgtaagaatcaagagtc 1288
|||||
Db 423 TATACTTACCAAGTAGAGGGCCGTGACACTTATGAATGCTGTGAAGATCAAGATGCTCC 482
|||||
Qy 1289 tggaaactcagatgacccctcctcagacacaattgaacgtacagggcaacagcaagc 1348
|||||
Db 483 TGGAACTCATGCAAGTACCTCTCCAGACACATTTGAACGATACAGGCAACGACACG 542
|||||
Qy 1349 agcagcaccagcacttacttcagaaca 1376
|||||
Db 543 AGCAGCACCAAGAGCTTACTTACGAACA 570
|||||

RESULT 3
LOCUS AM368377 636 bp mRNA EST 04-FEB-2000
DEFINITION PM2-HT0190-081099-001-c08 HT0190 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM368377
VERSION AM368377.1 GI:6873027
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM2&t2=PM2-HT0190-
081099-001-c08&t3=1999-10-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 635.
Location/Qualifiers
1. 636
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lb="HT0190"
/dev_stage="Adult"
/note="Organ: head,neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 139 a 150 c 155 g 192 t
ORIGIN
Query Match 18.1%; Score 511; DB 115; Length 636;
Best Local Similarity 99.0%; Pred. No. 4.5e-126;
Matches 514; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

858 agatccatcacaggaagacagagatgtgtgtacctatagaccacccaggttgac 917
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Db 629 AATCCATCAGAGAGACAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 570
 QY 918 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 977
 Db 569 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 510
 QY 978 CCGCGTCCATTTATGATGCTGCTTATGAGCCACCTCAGTTGGCAG 1037
 Db 509 CCGCGTCCATTTATGATGCTGCTTATGAGCCACCTCAGTTGGCAG 450
 QY 1038 ACCTGCTTGTGAGGCGGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1097
 Db 449 ACCTGCTTGTGAGGCGGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 390
 QY 1098 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1157
 Db 389 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 330
 QY 1158 GTTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1217
 Db 329 GTTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 270
 QY 1218 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1277
 Db 269 TGAATCAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 210
 QY 1278 CAAAGAGTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1337
 Db 209 CAAAGAGTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 150
 QY 1338 ACAAGAGTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1376
 Db 149 ACAAGAGTGTGCTGAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 111
 RESULT 4
 AM368375/6 637 bp mRNA EST 04-FEB-2000
 LOCUS PM2-HT0190-081099-001-a07 HT0190 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM368375
 ACCESSION AM368375.1 GI:6873025
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 637)
 AUTHORS HGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM2&t2=PM2-HT0190-
 081099-001-a07&t3=1999-10-08&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 14
 High quality sequence stop: 589.
 Location/Qualifiers
 1..637
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0190"
 /dev_stage="Adult"
 /note="Organ: head_neck; Vector: puc18; site_1: SmaI;
 site_2: SmaI; A mini-library was made by cloning products

BASE COUNT 136 a 146 c 161 g 194 t
 ORIGIN
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research).
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 Query Match 17.2%; Score 485; DB 115; Length 637;
 Best Local Similarity 98.8%; Pred. No. 4.3e-119;
 Matches 499; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 QY 872 GAAGAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 931
 Db 628 GGAGAGAGTGTGCTTATGAGCCACCTCAGTTGGCAG 570
 QY 932 TCTGTACATTTATGATGCTGCTTATGAGCCACCTCAGTTGGCAG 991
 Db 569 TCTGTACATTTATGATGCTGCTTATGAGCCACCTCAGTTGGCAG 510
 QY 992 TATCATTTGCTGCTGCTTATGAGCCACCTCAGTTGGCAG 1051
 Db 509 TATCATTTGCTGCTGCTTATGAGCCACCTCAGTTGGCAG 450
 QY 1052 CCGGATCTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1111
 Db 449 CCGGATCTGTGCTTATGAGCCACCTCAGTTGGCAG 390
 QY 1112 AGCAAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1171
 Db 389 AGCAAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 330
 QY 1172 CCAATGCTGCTGCTTATGAGCCACCTCAGTTGGCAG 1231
 Db 329 CCAATGCTGCTGCTTATGAGCCACCTCAGTTGGCAG 270
 QY 1232 ACTTACAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1291
 Db 269 ACTTACAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 210
 QY 1292 AACTCAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1351
 Db 209 AACTCAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 150
 QY 1352 AGCAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 1376
 Db 149 AGCAGAGTGTGCTGCTTATGAGCCACCTCAGTTGGCAG 125
 RESULT 5
 AM368378 514 bp mRNA EST 04-FEB-2000
 LOCUS PM2-HT0190-081099-001-d01 HT0190 Homo sapiens cDNA, mRNA sequence.
 DEFINITION AM368378
 ACCESSION AM368378
 VERSION AM368378.1 GI:6873028
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 AUTHORS HGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL:
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM2&t2=PM2-HT0190-081099-001-d01&t3=1999-10-08&t4=1>)

Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 514.

FEATURES

SOURCE

1. 514

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0190"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 147 a 113 c 141 g 113 t

ORIGIN

Query Match 17.2%; Score 483; DB 115; Length 514;
Best Local Similarity 98.8%; Pred. No. 1.4e-118;
Matches 497; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 771 gctgagcgtgaattcaacgagggagacagatgcctcctagtcattgattcagtaga 830

DB 2 GCGACCCCTGATTCACAGAGGACAGATTCGCCCTCCAGCATTTGATTCAGATAGA 61

QY 831 ggggaacacacatgcccacatgtatagaagatcccatcacagagaagacagatgtgtgt 890

DB 62 GGGGAACAGCCATGCCCAGATGTAGAAGATCCCATCAAGAGACAGAGTGTGTGT 121

QY 891 acctatgagccacccacaggttgcacgtcaattcaacagacgtctgtacatttcagt 950

DB 122 ACCTTATGAGCCACCCAGGTTGGCAGTCAATTCACAGACAGTTCATTCATGTG 181

QY 951 taacagcagttgtgttggagggatgaacgcgtcccaatttaattcattgtacttga 1010

DB 182 TACACACAGATGTTGGAGGGATGAGACCGCGCTCCCAATTTAATCATTTGACTGTGA 241

QY 1011 aaccagaagatggcgaagtccttggcgacgctgcttggagcccgatatttggctggcc 1070

DB 242 AACCAAGATGGCAGTCTGGGCCGACGCTGCTTTGAGGCCGGAATCTGTGTCGA 301

QY 1071 aggaagagacaggaagcgagatgaatagcatcagaagaacagcaagtttcgagacgtac 1130

DB 302 AGGAAGAGACAGGAAGCGGATGATGATGATGATGATGATGATGATGATGATGATG 361

QY 1131 aaagaacggtgtgtgtgaagaagccgcttctgcagaacacacatgtatcagatgtac 1190

DB 362 AAAGAACGGTGTGTGACAGAGCCGCTTCTGCTCAGAACACACATGATGATGATGATG 421

QY 1191 atccatcaagaagaagatcccatgagatgagacgttatacttccagttagggcg 1250

DB 422 ATCCATCAAGAAACGAGATTCCTCCAGATGATGATGATGATGATGATGATGATGATG 480

QY 1251 tgaagactatgaagtcgttga 1273

DB 481 TGAGACTTATGCAATGCTGCTGA 503

RESULT 6

AM382125

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

517 bp mRNA

CMO-HT0322-201299-135-e02 HT0322 Homo sapiens

AM382125

AW382125.1 GI:6886784

EST.

human.

EST

04-FEB-2000

CDNA, mRNA sequence.

EST.

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 517)

AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.brThis sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-HT0322-201299-135-e02&t3=1999-12-20&t4=1>)Seq primer: puc 18 forward
High quality sequence start: 38
High quality sequence stop: 517.

BASE COUNT 146 a 123 c 140 g 108 t

ORIGIN

FEATURES 1. 517

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="HT0322"

/dev_stage="Adult"

/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;

Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 146 a 123 c 140 g 108 t

ORIGIN

Query Match 16.6%; Score 467; DB 115; Length 517;
Best Local Similarity 95.7%; Pred. No. 2.8e-114;
Matches 506; Conservative 0; Mismatches 10; Indels 13; Gaps 2;

QY 680 caccctccagagagcgttaccgcgcacatcgcgtctacaaaaaagctgacgcgtca 739

DB 1 CAACCTCCTCGGAGACTGTATCCGCGCATCTCTGTACAAAAGCTGACGACGTCA 60

QY 740 cgaagtggtgaagcgtgtcccaacatgagctgagccgtgaattcaacgagggacaga 799

DB 61 CGAGGTGTTGAAGCGGTGCCCAACCATGAGCTGAGCCGTGAATTCAGAGGACAGA 120

QY 800 ttgcccctctcgtatcatttgatgagtagagaggaagacacatgcccagratgtagaag 859

DB 121 TTGCCCTCTCTGATATTTGATTCAGTAGAGGGAGAACGCCATGCCATGTGTAGAG 180

QY 860 atcccatcagaagaagagtgctgtgtacctaataagaccacccaggttgcagctg 919

DB 181 ATCCCATACAGAGAGAGAGATGTGTGATCTTATGAGCACCCAGGTTGGCACTG 240

QY 920 aattcagacagtcctgtac-aattcatgttcaacagcagttgtgttggaggtgaac 978

DB 241 AATTTCAGCAGACTGTTGTACAAATTTCAATGTTACAGAGTTGTGTAGAGGATGAC 300

QY 979 cgcgtccaatattatattatgttactctcggaaacacagatggcgaagtcctggccga 1038

DB 301 CGCCGTCCAATTTTATATCTTGTACTGTGAAACAGAGATGGCAAGTCTGTGGCCGA 360

QY 1039 cgcgtcttgaagcccgagtcgtgtcttgcaggaagaagacaggaagcgagatagaat 1098

DB 361 CGCTGCTTTGAGGCCCGAGATCTGTGCTTCCAGAGAGAGAGAGAGCGGATGAAT 420

QY 1099 agcatcagaagaacagatttcgagacagtacaagaacggtgtgttgaagcgcccg 1158

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Db      421 AGCATCAGAAACAGCAGTTCGACACTACAAAGACGGTGATG-----CG 468
Qy      1159 ttctgtcagaacacacatggtatccagatgacatccatcaagaacgaa 1207
          |||||
Db      469 TTTGCGTACAGACACACTATGATCCAGATGACATCCATCAGAAACGAA 517

RESULT 7
LOCUS   A1809318      498 bp      mRNA      EST      18-DEC-1999
DEFINITION we6a04.x1 Soares_NFL.T.GBC.S1 Homo sapiens cDNA clone
IMAGE:2348910 3', mRNA sequence.
ACCESSION A1809318
VERSION   A1809318.1 GI:5395884
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 498)
AUTHORS   NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          This clone is available royalty-free through LNL; contact the
          IMAGE Consortium (info@image.lnl.gov) for further information.
          Insert length: 1013 Std Error: 0.00
          Seq primer: -400P from Glibco
          High quality sequence stop: 446.
FEATURES
  source
    1..498
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    /db_xref="taxon:9606"
    /clone_image="2348910"
    /clone_lib="Soares_NFL.T.GBC.S1"
    /lab_host="DH10B"
    /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
    a modified polylinker; Site.1: Not I; Site.2: Eco RI;
    Equal amounts of plasmid DNA from three normalized
    libraries (fetal lung NBHL19W, testis NHT, and B-cell
    NCI-CGAP-GCBI) were mixed, and ss circles were made in
    vitro. Following HAP purification, this DNA was used as
    tracer in a subtractive hybridization reaction. The driver
    was PCR-amplified cDNAs from pools of 5,000 clones made
    from the same 3 libraries. The pools consisted of
    I.M.A.G.E. clones 297480-302087, 682632-687239,
    726408-728711, and 729096-731399. Subtraction by Bento
    Soares and M. Fatima Bonaldo."
BASE COUNT 172 a 73 c 100 g 153 t
ORIGIN
Query Match 16.1%; Score 452.4; DB 102; Length 498;
Best Local Similarity 97.0%; Pred. No. 2.3e-110;
Matches 483; Conservative 0; Mismatches 11; Indels 4; Gaps 2;

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Qy      2558 aagatgaaagggtagactactttctttttta--ctcaaaagtttagaactctg 2615
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Db      258 AAGATGAAAGGAGTAGACTACTTTCTTTTAACTCAAAAAGTTAGAACTCTG 199
          |||||
Qy      2616 ttctcttcattttaaaacatatattagaataatagataaagactttaaaagtcc 2675
          |||||
Db      198 TTTCTTTTCATTTTAAACATATATTTTAAAGATATAGCTAAAGACTTTTAAATGTTTC 139
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Qy      2676 tcccccacatctccacacccagctacacagacgtattctctgcacacagacga 2735
          |||||
Db      138 TCCCTCCATCTTCCACACCCAGTACACGACGATATTTCTGTCCACCAAGACATTA 79
          |||||
Qy      2736 ttctctgtatcgaagcgtctgctttgtgat-9gtgacttcaatttcaataact 2793
          |||||
Db      78 TTTCTGTATATGAGCGCTGTGCTTAGTAATCCGCGATATTTTAAATTTCAATTAAC 19
          |||||
Qy      2794 ttgcatcttggttaaa 2811
          |||||
Db      18 TTTGCAATTTGTTTAAAA 1

RESULT 8
LOCUS   BF774398      450 bp      mRNA      EST      12-JAN-2001
DEFINITION 284057 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF774398
VERSION   BF774398.1 GI:12122298
KEYWORDS  EST.
SOURCE    cow.
ORGANISM  Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 450)
AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
          Bennett,G.A., Fahrnerkrug,S.C., Fekling,B.A., Rohrer,G.A., Laegreid
          ,W.W. and Keele,J.W.
          Design and use of four pooled tissue normalized cDNA libraries for
          EST discovery in cattle
JOURNAL   Unpublished (2000)
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smithemail.marc.usda.gov
          Single pass sequencing. Bases called and alt-trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -mnscore 18
          and -mismatch 12 options.
          PCR Primers
          FORWARD: AGGAACAGCATATGACCAT
          BACKWARD: GTTTCGAGTCACGACG
          Plate: 83 row: C column: 20
          Seq primer: ATTTAGTGACACTATAG.
FEATURES
  source
    1..450
    /organism="Bos taurus"
    /db_xref="taxon:9913"
    /clone_lib="MARC 3BOV"
    /tissue_type="pooled"
    /lab_host="DH10B"
    /note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
    library made from pooled tissue from marrow, alveolar
    macrophage, ovary, fetal semitendinosus muscle, and fetal
    longissimus muscle."
BASE COUNT 130 a 122 c 113 g 85 t
ORIGIN
Query Match 14.5%; Score 408.4; DB 169; Length 450;
Best Local Similarity 94.2%; Pred. No. 1.5e-98;
Matches 424; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

```

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QY 1020 tgggcaagtcctgggcccagcgtcttgaggcccgatctgtctgcccagaaga 1079
Db 1 tgggcaagtcctgggcccagcgtcttgaggcccgatctgtctgcccagaaga 60
QY 1080 cagggaagcgatgaagatagatcagaagcaagcttgaggcaagtaagaaga 1139
Db 61 cagggaagcgatgaagatagatcagaagcaagcttgaggcaagtaagaaga 120
QY 1140 tgaatgtaagacgcccgtcttcagacaacatggtatccagatgacatccatca 1199
Db 121 tgaatgtaagacgcccgtcttcagacaacatggtatccagatgacatccatca 180
QY 1200 gaaacgaagatcccaagatgatactgtatacttaacagtgaggcgctgagacta 1259
Db 181 gaaacgaagatcccaagatgatactgtatacttaacagtgaggcgctgagacta 240
QY 1260 tgaatgctgtgaagataaagaagtcctggaactcatgacatcttcctcagaacac 1319
Db 241 cgaatgctgtgaagataaagaagtcctggaactcatgacatcttcctcagaacac 300
QY 1320 aattgaacgtacagcaacagcaacagcaacagcaacagcaacagcaacagcaac 1379
Db 301 gattgaacgtacagcaacagcaacagcaacagcaacagcaacagcaacagcaac 360
QY 1380 ccttcagcgtcttcagagatgactgttgagcccgagagagaaactccaaacaatc 1439
Db 361 ccttcagcgtcttcagagatgactgttgagcccgagagagaaactccaaacaatc 420
QY 1440 tgaagtccttcagacatcccaagcccc 1469
Db 421 tgaagtccttcagacatcccaagcccc 450

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```

RESULT 9
LOCUS BE752074 541 bp mRNA EST 15-SEP-2000
DEFINITION 204371 MARC 280V Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE752074
VERSION BE752074.1 GI:10160606
KEYWORDS EST.
SOURCE Bos taurus
ORGANISM Bos taurus; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 541)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keefe,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTCACGACG
Plate: 45 row: M column: 16
Seq primer: ATTGAGTGACACTATG.
FEATURES
Source
1. 541
Location/Qualifiers
/organism="Bos taurus"
/db_xref="taxon:9913"
/cisue_lib="MARC 280V"
/tissue_type="pooled"

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/lab host="DH10B"
/note="Vector: PCMV SPOR6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 149 a 132 c 133 g 127 t
ORIGIN

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Query Match 14.4%; Score 406; DB 139; Length 541;
Best Local Similarity 90.6%; Pred. No. 6.9e-98;
Matches 433; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 1086 ggcgatgaagatagatgacatcagaagagcagcaagcttcgagacgtacagaagcgtgtag 1145
Db 1 ggcgatgaagatagatgacatcagaagagcagcaagcttcgagacgtacagaagcgtgtag 60
QY 1146 tacgaagcgccgtcttcagacaacatggtatccagatgacatccatcaagaagc 1205
Db 61 tacgaagcgccgtcttcagacaacatggtatccagatgacatccatcaagaagc 120
QY 1206 aagatcccaagatgatactgtatacttaacagtgaggcgctgagactgagaaat 1265
Db 121 aagatcccaagatgatactgtatacttaacagtgaggcgctgagactgagaaat 180
QY 1266 gctgtgaagatcagaagtcctcgaactcatgacatcttcctcagaacacatgta 1325
Db 181 gctgtgaagatcagaagtcctcgaactcatgacatcttcctcagaacacatgta 240
QY 1326 aacgtacagcaacagcaacagcaacagcaacagcaacagcaacagcaacagcaac 1385
Db 241 aacgtacagcaacagcaacagcaacagcaacagcaacagcaacagcaacagcaac 300
QY 1386 agcctgcttcagagatgactgttgagcccgagagagaaactccaaacaatcagct 1445
Db 301 agcctgcttcagagatgactgttgagcccgagagagaaactccaaacaatcagct 360
QY 1446 ctcttcagacatcccaagcccccaaccagatcagtgataagacagccctatctat 1505
Db 361 ctcttcagacatcccaagcccccaaccagatcagtgataagacagccctatctat 420
QY 1506 atttaagtgctgtgtgtatcttcacatgtagatgtagtggtgtgtgtgtgtgtgt 1563
Db 421 atttaagtgctgtgtgtatcttcacatgtagatgtagtggtgtgtgtgtgtgtgtgt 478

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```

RESULT 10
LOCUS AW379296 508 bp mRNA EST 04-FEB-2000
DEFINITION MR0-HT0241-091293-004-b02 HT0241 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379296
VERSION AW379296.1 GI:6883955
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS HCGP http://www.judwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@judwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.judwig.org.br/scripts/gethtml2.pl?l=MR0&t2=MR0-HT0241-
091293-004-b02&t3=1999-12-09&t4=1)

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Db 544 GACCATACCGGAGACAGGCTCTGAATGAAGTACACCAAAAATGAGACTCCAGC 603
 Oy 1150 aagagcccgcttcgtcagaacacacatggtat-----ccagatgacatccatcaagaa 1203
 Db 604 AAGCGTGATTCAGACAGAGCCCTCCATCCCTGCGCTGGTACCACTGAAGAG 663
 Oy 1204 cgaagatcccccagatgaaactgtatcacttaccgtgagggcgagagactaata 1263
 Db 664 AGACGCCAGCGGAGAGAGACATGTTCTACATGCAGCGCGGCGGAGAGACTTTGAG 723
 Oy 1264 atgctgttgaagatcaaaagatccctggaactcagtcacttccctcagacacaatt 1323
 Db 724 ATCTTGATGAAGTCAAGAGAGCTAGATGATGAGCTTGCCCAAGCTTTGGTT 783
 Oy 1324 gaacgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1383
 Db 784 GACGCTCTATCGACAGCAGCAGCAGCAGCTCTCTACAGAGCGCGAGTCACTGAGCCT 843
 Oy 1384 tcagcct 1390
 Db 844 CCATCCT 850

RESULT 13

AM379300 565 bp mRNA EST 04-FEB-2000
 LOCUS MRO-HT0241-101299-003-a05 HT0241 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM379300
 VERSION AM379300.1 GI:6883959
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 565)
 AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?rl-MR0<2-MR0-HT0241-101299-003-a05<3-1999-12-10<4-1>)
 Seq primer: puc 18 forward
 High quality sequence start: 52
 High quality sequence stop: 331.
 Location/Qualifiers

FEATURES

source
 1. 565
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HT0241"
 /dev_stage="Adult"
 /note="Organ: head_neck; Vector: puc18; Site:1: Sma1;
 Site:2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 Profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."
 BASE COUNT 178 a 126 c 140 g 121 t
 ORIGIN

Query Match 13.7%; Score 385.6; DB 115; Length 565;
 Best Local Similarity 95.7%; Pred. NO. 2.1e-92;
 Matches 440; Conservative 0; Mismatches 14; Indels 6; Gaps 4;

Oy 923 tcacgacagctctgtacacatttcacatgtgttaaca-gcagttgtgttgagggatgaaccgc 981
 Db 7 TCACGACAGCTCTGTGAGATTTTCATGTGTAAACACCAGTGTGTGGAGGATGAACGC 66
 Oy 982 cgtccaatltaacatcattgttactctgtgaaacagagatgtgcaagtcctgtgcccagc 1041
 Db 67 CGTCCAAATTTTATATCTTGTCTCTGGAACCAAGATGGCAAGTCTGTGGCCGAGCG 126
 Oy 1042 tgcctttagggcccgagatcgtgtgttgccttgccttgccttgccttgccttgccttgc 1101
 Db 127 TGCTTTGAGGCCCGGATGCTGTCTTGCAGAGAGACAGAGAGAGGCGGATGAATAGC 186
 Oy 1102 atcgaagaagcgaagatgttcgacagcagtcagaagaacggtgtatgtgtacgaagccgctt 1161
 Db 187 ATCAGAAAGCAGCAAGTTTGGACAGTACAAAGAGGATGATGATGAGAGCGCGCTT 246
 Oy 1162 cgtcagaacacacatgtatcag--atgacatccatcaagaacgaagatccacagatg 1219
 Db 247 CGTCAAGACACACATGTTATCCAGATGACCATCCATCAGAAACGAGATCCCAAGATG 306
 Oy 1220 atgaacttacttacttaccagtgagggcggtgagact--atgaactgtgtgaagat 1277
 Db 307 ATGAAGTGTATCTTACACAGTGAAGGCGCGGAGACTTTATGAACATGCTGTGAAGAT 366
 Oy 1278 caaagaagtccttcggaactcattcagttacttctccta-gaaccaattgaagctcagc 1336
 Db 367 CAAAGAGTCCCTGGAGACATCATCTTCACTTCTCAGGAAACATTTGAAGTACAGGC 426
 Oy 1337 aacgacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1376
 Db 427 AACAGCACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 466

RESULT 14

AA739350 532 bp mRNA EST 14-JAN-1998
 LOCUS v51g01.r1 Soares_thymus_2nbwt Mus musculus cDNA clone
 DEFINITION IMAGE:1225968 5', mRNA sequence.
 ACCESSION AA739350
 VERSION AA739350.1 GI:2775536
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 532)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Giesel,S., Kucab,L., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mousetest@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:651560
 Seq primer: -28m3 rev2 ET from Amersham
 High quality sequence stop: 508.
 Location/Qualifiers

FEATURES

source
 1. 532
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="IMAGE:1225968"
 /clone_lib="Soares_thymus_2nbwt"

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/sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/Note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGAGCGCGGTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M. Fatima Bonaldo."

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```

BASE COUNT      142 a      142 c      126 g      122 t
ORIGIN
Query Match      13.5%; Score 380.2; DB 11; Length 532;
Best Local Similarity 84.4%; Pred. No. 5.8e-91;
Matches 453; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

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OY 1141 gatgtgacgaagcccgcttctgcaagaacacatggtatccagatgacatcatcaag 1200
|||||
DB 1 GATGTGACGAAGCGCCCTTCCGTGAGATACACAGGATCCAGATCCATCCATCAAG 60
OY 1201 aaaggaagatcccaagatataactgtatactaccagtgaggccgtgaactat 1260
|||||
DB 61 AAACGGAGATCCCGAGATATAGCTGCTGTAACCTACAGTACAGAGGTGTACAGCATAC 120
OY 1261 gaatgctgttgaagaacaaagctccctgaactaatgactactcctccagacaca 1320
|||||
DB 121 GAGATGCTTCTGAGATCAAGATCAAGATCAGATCAGATCAGATCAGATCAGATCAG 180
OY 1321 attgaagctacaggaacagcaagcagcagcagcagcagcagcagcagcagcagc 1380
|||||
DB 181 ATCGAAGCTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 240
OY 1381 cttagagctgtctcaggaatgagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
|||||
DB 241 CTTTACGCTGCTTCAAGATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
OY 1441 gaagctctcttgaagaacaaagcccaaacagcagcagcagcagcagcagcagcagc 1500
|||||
DB 301 GAGCTTCTTGTAGATTCACAAACCCCAACCACTCGTGTACCATAGATGAGTCCAGC 360
OY 1501 tctaatcttaagtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
|||||
DB 361 TATGTGTT-----TGAGTTCAATGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 415
OY 1561 tctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1620
|||||
DB 416 CATGCTGTTAGTGTTCACAGCCCTTCAACAACAGACTGTGAAGACATTTTGGCTCAGA 475
OY 1621 cccaactgtctcaaaaggaacaaagcactagtgagagaatcttttgaaggagactcaa 1677
|||||
DB 476 CACAGCTGCTCAAGGACACATCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 531

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```

RESULT 15
AM382186      507 bp      mRNA      EST      04-FEB-2000
LOCUS      CM0-HT0324-261199-101-e02 HT0324 Homo sapiens cDNA, mRNA sequence.
DEFINITION      AM382186
ACCESSION      AM382186
VERSION      AM382186.1 GI:6886845
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE      1 (bases 1 to 507)
AUTHORS      HCGP http://www.ludwig.org.br/ORESTES.
TITLE      The FAPESP/LICR Human Cancer Genome Project

```

```

JOURNAL      Unpublished (1999)
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?pl1=CM0&lt2=CM0-HT0324-
261199-101-e02&lt3=1999-11-26&lt4=1)
Seq primer: puc.18 forward
High quality sequence start: 27
High quality sequence stop: 398.
Location/Qualifiers

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```

FEATURES
SOURCE
1..507
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0324"
/dev_stage="Adult"
/Note="Organ: head,neck. Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

```

BASE COUNT      150 a      118 c      136 g      103 t
ORIGIN
Query Match      12.9%; Score 364.4; DB 115; Length 507;
Best Local Similarity 92.8%; Pred. No. 1e-86;
Matches 464; Conservative 0; Mismatches 16; Indels 20; Gaps 7;

```

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OY 716 tctcaaaaaagctgacgacgtcagcaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 775
|||||
DB 20 TCTCAAAAAAGCTGACGACGTCAGCGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 79
OY 776 gccgtgaattcaagaggaacagatgtccctctctagtcatttgattgagtaaggaga 835
|||||
DB 80 GCCGTGAATTCAACAGGAGACAGATTTGCCCTCTTATGATTTGATTTGATTTGATTTG 139
OY 836 acagcagatgcccagatgtagaagaatcccatcacagaagaagagtgctgtacctt 895
|||||
DB 140 ACAGCCATGCCAGATGTAGATATCCATCACAGAGACAGAGAGTGTGTGTGTGTGTGTGT 199
OY 896 atgaagcaccaccaagcttgacatgaattc-acagagctctgttac-aattcaatgttaa 953
|||||
DB 200 ATGAGCGACACCAGGTTGGCACTGAATTCACAGACAGCTGTGTACAAATTTTCATGTGTA 259
OY 954 cagcaggtgtgtgtgaagagatgaaccggttcaatttaattcaattgttacctt--ggaa 1011
|||||
DB 260 CAGCAGTGTGTGTGAAGGATGAACCCCGTCAATTTTAATCATTTGACTTTGGAAA 319
OY 1012 accagagatggcgaagctcctggcagcgtgcttcttgaggcccgatctgtgtgccca 1071
|||||
DB 320 ACCAGAGATGGGCAAGTCTCTGGAGAGAGCGCTCTTAAGAGGCCGATCTGTGTGTGTGT 379
OY 1072 ggaagag--acaggaagcgcgataagataagataagaagaagcagaatttcgcagata 1129
|||||
DB 380 GGAAGAGCACAGAGACAGCGGATCAAGATACATCAAGAACAGCACTTTTCGGACATA 439
OY 1130 c-aagaagacggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1187
|||||
DB 440 CAAAGAACGGTGATG-----CGTATCGTCAAGAACACACATTTGTATCAAT 487
OY 1188 gacatccatcaagaagaagaa 1207
|||||
DB 488 GACATCATCAAGAAACGAA 507

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Wed Aug 8 08:03:56 2001

us-09-670-568b-2.rst

Page 13

Search completed: August 7, 2001, 22:52:06
Job time: 8102 sec

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